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1462.883 Million cell updates/sec
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AJ717397 Schedonor
AJ717396 Schedonor
AJ7186400 Schedonor
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AE013459 Methanosa
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AC005777 Homo sapi
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AL139926 Human DNA
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BC002875 Homo sapien
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Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales;
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Method and kit for identifying vancomycin-resistant enterococcus
Patent: WO 2005028679-A 4 31-MAR-2005;
University of Iowa Research Foundation (US); DODGSON, Kirsty Janu
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/mol_type="unassigned DNA"
/db_xref="taxon:1352"
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AC141676 Apis mell
AC087274 Homo sapi
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AC156177 Bos tauru
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AC117890 Rattus no
AC1037256 Rattus no
AC103121 Rattus no
AC095111 Rattus no
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Inouye,R.T., Torres-Viera,C., Moellering,R., Gold,H. and Eliopoulos,G.M.
Methods and compositions for restoring antibiotic suscep glycopeptide-resistant Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COURVALIN
PC C12N15/
C12N5/10,
                                                                                                 Enterococcus faecium
Enterococcus faecium
Bacteria; Pirmicutes;
                                                                                                                                                                  AX085668
AX085668.1 GI:13275654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 1029)
Arthur, M., Duktammalen, S., Molinas, C. and Courvalin, P.
Polypeptides implicated in the expression of resistance to
glycopeptides, in particular in gram-positive bacteria, nucleotide
sequence cod ing for these polypeptides and use for diagnosis
Patent: JP 2002320494-A 2 05-NOV-2002;
                                                                                                                                                                                                Sequence 21 from Patent
                                                                                                                                                                                                                   AX085668
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31-OCT-1990 FR 90/13579
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Pred. No. 7
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               for restoring antibiotic susceptibility in
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                                                                                                                                         Enterococcus faecium
Enterococcus faecium
Bacteria; Firmicutes;
                                                                                                                                                                                            CQ797595 1034 bp
Sequence 9 from Patent BP1408120.
CQ797595
CQ797595.1 GI:46425887
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Highly conserved genes and their use to generate probes and primer for detection of microorganisms
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Bacteria; Firmicutes; Lactobacillales; Enterococcaceae
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                                                                                  Detection of vancomycin-resistant Enterococcus spp
                                                                                                Cockerill, F.R. and Sloan, L.M.
                                                                                                                             encerococcus.
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Beth Israel Deaconess Medical Center
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                                                      nt: EP 1408120-A 9 14-APR-2004; FOUNDATION FOR MEDICAL EDUCATION
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ilarity 100.0%;
Conservative (
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                                           Location/Qualifiers
organism="Enterococcus faecium"
|mol_type="unassigned DNA"
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/mol_type="unassigned DNA"
/strain="BM4147"
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Enterococcus faecalis
Bacteria; Firmicutes; Lactobacillales;
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Highly conserved genes and their use to generate probes and primers for detection of microorganisms
Patent: WO 0123604-A 1055 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
Location/Qualifiers
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Enterococcus gallinarum
Bacteria; Firmicutes; Lactobacillales;
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                                                                  Bergeron,M.G., Boissinot,M., Huletsky,A., m picard,F.J. and Roy,P.H.
Highly conserved genes and their use to gene for detection of microorganisms patent: WO 0123604-A 1054 05-APR-2001; Infectio Diagnostic (I.D.I.) INC. (CA) Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Enterococcus gallinarum"
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                     mol_type="unassigned DNA"
db_xref="taxon:1351"
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 l Similarity
20; Conserv
                                                                                                                             Highly conserved genes and their use to for detection of microorganisms Patent: WO 0123604-A 1049 05-APR-2001; Infectio Diagnostic (I.D.I.) INC. (CA)
                                                                                                                                                                                                                         Enterococcus faecium
Enterococcus faecium
Bacteria; Firmicutes;
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Bacteria; Firmicutes;
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/strain="R492"
/db_xref="taxon:1352"
                                                        /mol_type="unassigned
/strain="R690"
/db_xref="taxon:1352"
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Pred. No. 7.3;
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Pred. No. 7.3;
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Pred. No. 7.3;
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Highly conserved genes and their use to generate probes and primer; for detection of microorganisms patent: WO 0123604-A 1053 05-APR-2001; Infectio Diagnostic (I.D.I.) INC. (CA)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                    Enterococcus faecium
Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
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Highly conserved genes and their use to for detection of microorganisms
Patent: WO 0123604-A 1050 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
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Sequence 1053 from Patent WO0123604.
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Enterococcus gallinarum
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
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Conservative
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                                                                                                                                /mol_type="unassigned DNA"
/strain="R581"
                                                                                                                db_xref="taxon:1352"
                                                                                                                                                            organism="Enterococcus faecium"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Enterococcus gallinarum"
/mol_type="unassigned DNA"
/strain="R691"
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                                                                                                                                                                                                                                                                                                                             Enterococcus flavescens
Enterococcus flavescens
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
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Highly conserved genes and their use to generate probes and primers for detection of microorganisms
Patent: WO 0123604-A 1056 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
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                                                     Similarity 100.
20; Conservative
                                                                                                                                                                                                                                                                                                                  Enterococcus.
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1056 from Patent WO0123604.
                                                                                                                       /organism="Enterococcus flavescens"
/mol_type="unassigned DNA"
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                                                                                                                                                                                                Location/Qualifiers
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                                                                   100.0%; Score 20; DB 6; 100.0%; Pred. No. 7.3;
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1 (bases 1 to 1768)

1 (bases 1 to 1768)

Dutka-Malen,S., Molinas,C., Arthur,M. and Courvalin,P.

The VANA glycopeptide resistance protein is related to D-alanyl-D-alanine ligase cell wall biosynthesis enzymes Mol. Gen. Genet. 224 (3), 364-372 (1990)
                                                                                                                                                                                 Direct Submission
Submitted (25-FEB-1991) S. Dutka-Malen, Institut Pasteur, Agents Antibacterions, 28 rue du Dr Roux, Paris Cedex 15,
                                                                                                                                                                                                                                                                                                                                                     Enterococcus faecium
Enterococcus faecium
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E.faecium plasmid pIP816 vanA
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Enterococcus faecium
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Sequence 1051 from
AX110318
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ilarity 100.0%;
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                                                    /gene="vanA"
377. .1408
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/mol_type="unassigned DNA"
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/codon_start=1
/evidence=experimental
/transl_table=11
                                    /gene="vanA"
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                                                                                                 plasmid="pIP816"
                                                                                                                          mol_type="genomic DNA"
strain="BM4147"
                                                                                                                                                  organism="Enterococcus
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CQ797597.1
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Cockerill, F.R. and Sloan, L.M. Detection of vancomycin-resistant Ente Patent: Ep 1408120-A 11 14-APR-2004; MAYO FOUNDATION FOR MEDICAL EDUCATION
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Bacteria; Firmicutes,
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KKIYKALGCRGLARVDMFLQDNGRIVLNEVNTLPGFTSYSRYPRMMAAAGIALPELID
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                                                                         Highly conserved genes and their use to generate probes and primers for detection of microorganisms
Patent: WO 0123604-A 1139 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
                                                                                                                                                                                                                                                                                   Sequence 1139 from Patent WO0123604. AX110406
                                                                                                                                        Bergeron, M.G., Boissinot Picard, F.J. and Roy, P.H.
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Sequence 1 from Patent WO2005028679.
CS061873
                                                                                                                                                                                                                      Enterococcus faecium
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Enterococcus faecium
                                                                                                                                                                                                   Bacteria; Firmicutes; Lactobacillales; Enterococcaceae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dodgson, K.J.
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/mol_type="unassigned DNA"
/strain="BM4147"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Enterococcus faecium"
/mol_type="unassigned DNA"
/db_xref="taxon:1352"
                              organism="Enterococcus faecium"
                                                          ocation/Qualifiers
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db_xref="taxon:1352"
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100.0%; Pred. No. 7.4;
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Bergeron,M.G., Ouellette,M. and Roy,P.H.
Species specific and universal DNA probes and amplification primers to rapidly detect and identify common bacterial pathogens and associated antibiotic resistance genes from clinical specimens for routine diagnosis in microbiology laboratories
Patent: US 6001564-A 170 14-DEC-1999;
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AR089411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bergeron, M.G., Picard, P.J., Ouellette, M. and Roy, P.H. Species-specific and universal DNA probes and amplification primers to rapidly detect and identify common bacterial pathogens and associated antiblotic resistance genes from clinical specimens for routine diagnosis in microbiology laboratories
Patent: US 5994066-A 170 30-NOV-1999;
                                                                                                                                                                                                                                                                                              Unknown
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                                                                                                                                                                                                                                                                                                                                                       Sequence 170 from patent US 6001564. AR093611
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Bergeron, M.G.,
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                                                                                                                                                                  Location/Qualifiers
                                                                                                                      /organism="unknown"
/mol_type="unassigned DNA"
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ACCESSION
                                                                                                                                                                                                                                 AUTHORS Arthur, M., DuktaMmalen, S., Molinas, C. and Courvalin, P.

Polypeptides implicated in the expression of resistance to glycopeptides, in particular in gram-positive bacteria, nucleotide sequence cod ing for these polypeptides and use for diagnosis TOURNAL Patent: JP 2002320494-A 11 05-NOV-2002;

ENT OS Bacteria
PN JP 2002320494-A/11
PD 05-NOV-2002
PF 21-ESB-2002 JP 2007-
PR 31-CCT-1007
PR 31-CCT-1007
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Sequence
AR035514
                                                                                                                             PC C12N15/09,C07K14/315,C07K16/12,C12N1/15,C12N1/15,C12N1/15,C12N1/15,C12N1/15,C12N1/15,C12N1/15,C12N1/15,C12N1/15,C12N1/15,C12N1/108,PC C12Q1/04,C12Q1/68,G01N33/53,G01N33/566,G01N33/569//C12P21/08,PC (C12Q1/04,C12R1:01),C12N15/00,C12N15/00 CC Polypepides implicated in the expression of resistance to CC Polypepides implicated in the expression of resistance to CC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arthur,M., Dukta-Malen,S., Molinas,C. and Courvalin,P. Probes for the detection of nucleotide sequences implicated expression of resistance to glycopeptides, in particular in gram-positive bacteria
Patent: US 5871910-A 17 16-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BD181855
POlypeptides implicated in the expression of resistance to glycopeptides, in particular in gram-positive bacteria, nuclectide sequence cod ing for these polypeptides and use for diagnosis.
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                                                               in particular in gram-positive bacteria, cod ing for these polypeptides and use for diagnosis Key Location/Qualifiers
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/organism='Bacteria'
Location/Qualifiers
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2 (bases 1 to 7225)

2 (continue of policy of mucleotide sequences implicated expression of resistance to glycopeptides, in particular in gram-positive bacteria

2 (continue of policy of poli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bergeron, M.G., Boissinot Picard, F.J. and Roy, P.H.
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Bacteria; Firmicutes; Lactobacillales;
                                                                                                                                                                                                                                                                                                                    Unclassified
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/mol_type="unassigned DN
/strain="BM4147"
/db_xref="taxon:1352"
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                        /organism="unknown"
/mol_type="unassigned DNA"
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Enterococcus faecium transposon Tn1546 transposase, resolvase,
(vanR), vanS (vanS), vanH (vanH), vanA (vanA), vanX (vanX), van
(vanY), and teicoplanin resistance protein (vanZ) genes, comple
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C12N5/10,
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Arthur,M., DuktaMmalen,S., Molinas,C. and Courvalin,P.
Polypeptides implicated in the expression of resistance to
glycopeptides, in particular in gram-positive bacteria, nucleotide
sequence cod ing for these polypeptides and use for diagnosis
Patent: JP 2002320494-A 9 05-NOV-2002;
             Enterococcus faecium Enterococcus faecium
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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AUTHORS
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J. Bacteriol. 175 (1), 117-127 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arthur,M., Depardieu,F., Molinas,C., Reynolds,P. and Courvalin,P. The vanZ gene of Th1546 from Enterococcus faecium BM4147 confers
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Arthur, M., Molinas, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus,
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Gene 154 (1), 87-92 (1995)
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GLLHHETDLNI EEHYTDTAGYTDQI FGLTHLLGFKFAPRI RDLSDSKLFTI DKASEYP
KLEAI LRGQINTKVI KENYEDVLRLAHS I REGTVSASLI MGKLGSYSRQNSLATALRE
MGRI EKTI FILNY I SDESLRRKI QRGLNKGEAMNGLARA I FFGKQGELRERT I QHQLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEKVVSLNSLRPLKLS"
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1976. .4671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specimen_voucher="BM4147"
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AR035513
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FEATURES
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ORGANISM
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DEFINITION
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BD181854
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KEYWORDS
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AR035513
1 (bases 1 to 10851)
Arthur,M., DuktaMmalen,S., Molinas,C. and Courvalin,P.
Polypeptides implicated in the expression of resistance to
glycopeptides, in particular in gram-positive bacteria, nucleotide
sequence cod ing for these polypeptides and use for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 10851)
Arthur,M., Dukta-Malen,S., Molinas,C. and Courvalin,P.
Probes for the detection of nucleotide sequences implicated expression of resistance to glycopeptides, in particular in gram-positive bacteria
Patent: US 5871910-A 16 16-FEB-1999;
Location/Qualifiers
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                                                                                                    unidentified unidentified
                                                                                                                                                                                 10851 bp DNA linear PAT 15-MAY-2003 Polypeptides implicated in the expression of resistance to glycopeptides, in particular in gram-positive bacteria, nucleotide sequence cod ing for these polypeptides and use for diagnosis.
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                                                                                     unclassified
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Pred. No.
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Robert Koch Institute,

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C12N5/10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glycopeptide-resistant Enterococcus Patent: WO 0112803-A 1 22-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Methods and compositions for restoring antibiotic susceptibility in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inouye,R.T., Torres-Viera,C., Moellering,R., Gold,H. and
Bliopoulos,G.M.
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                                                                                                            TTCAGGCTCATCCTTCGGTG 7519
                                                                                                                                                  TTCAGGCTCATCCTTCGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                Israel Deaconess Medical Center,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15/10, C12Q1/04, C12Q1/68, G01N33/53, G01N33/566, G01N33/569//C12P21/08, C12Q1/04, C12R1:01), (C12Q1/68, C12R1:01), C12N15/00, C12N5/00 CC CC CC C12Q1/04, C12R1:01, C12Q1/68, C12R1:01), C12R15/00, C12R1:01, C12Q1/68, C12R1:01, C12R15/00, C12R1:01, C12Q1/68, C12R1:01, C12R15/00, C12R1:01, C12Q1/68, C12R1:01, C12R1:0
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                                                                                                                                                                                                            Conservative
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31-OCT-1990 FR 90/135
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                /mol_type="unassigned
/db_xref="taxon:1352"
                                                                                                                                                                                                                                                                                                                                                                                  organism="Enterococcus faecium"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 17510)
Werner,G., Klare,I. and Witte,W.
Multi-resistance gene cluster on a plasmid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF516335 17510 bp | I
Enterococcus faecium plasmid pUW786
gene cluster, complete sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterococcus faecium
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Location/Qualifiers
                                                                                                                                                                                                                      /codon_start=1
/transI_table=11
/product="truncated protein
/protein_id="AAM/7883.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'translation="MSDKILIVDDEHEIADLVELYLKNENYTVFKYYTAKEALECIDK
3BIDLAILDIMLPGTSGLTICQKIRDKHTYPIIMLTGKDTEVDKITGLTIGADDYITK
?PRPLELIARVKAQLRRYKKFSGVKEQNENVIVHSGLVINVNTHECYLNEKQLSLTPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="PSRQFQQLNEIGMDIIYEEKVSGATKDREQLQKVLDDLQEDDII
rvTDLTRITRSTQDLFELIDNIRDKKASLKSLKDTWLDLSEDNPYSQFLITVMAGVNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Enterococcus faecium"
product="pyruvate dehydrogenase"
                           codon_start=1
transl_table=11
                                                                                                                              gene="vanH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSILRILCENKGNVVSSELLFHEIWGDEYFSKSNNTITVHIRHLREKMNDTIDNPKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=1
transI_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product="putative resol'
protein_id="AAM77881.1"
                                                                                                                                                                              translation="MVIKLKNKKTTIPN"
                                                                                                                                                                                                                                                                                                                                                                                                                             gene="vanS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KTVWGVGYKIEK"
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transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene="vanR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transposon="Tn1546"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           db_xref="GI:21886738"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       db_xref="taxon:1352"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 roduct="cytoplasmic regulator"
rotein_id="AAM77882.1"
bb_xref="GI:21886739"
                                                                                                                                                                                                                                                                                                                             llele="vanS'"
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                                                                                                                                                                                                                                                                                                                                                                                                    lele="vanS'"
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RKKQGAFLINTGRGPL/DTYELVKALENGKLGGAALDVLEGEBEFFYSDCTQKFIDNQ
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GEDGSJQGLFELSGIPFVGCDJQSSAICMDKSITYIVAKNAGITPAFWYINKDDRPV
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Staphylococcus aureus plasmid
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AE017171.1 GI:33390917
Staphylococcus aureus
Staphylococcus aureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="ermB methylase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /insertion
9594. .9613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VBFLVTDMNAAYFQLTKRVLFNAKVVIDRFHIVKHMNQAFNELRIREMNELRKAGQKS
QAEKLKKNMRFLLKNRANINHYEYKTWKSFRAPKYPFLTEAMMIDRLLEFSPPLKEAY
PFFHELVEAFRDKDPDLFFSLLAELPETLDDSFREKLQNLLTYEEGITNAMIYPYSNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRSCGSTVVDGNGKAIIVKNGKKETIVRFEQYNHMPLVMRLKKQRYTCKNCRTHWTAQ
SYFVQPRHSIANHVRYKIASLLTEKVSLSFIAKSCQVSLTTVIRTLKEFKSYLPKQSK
KILPRVLMVDEFRSHASIEDKMSFICADGETGKLIDVLPTRKLPRLTSYFLGCTNPEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KIEAKNTHIKTMKRVSYGFKSFENMRIRIFLINQLINVR"
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                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="IR-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MLVFQMRNVDKTSTVLKQTKNSDYTDK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq="IS150-like"
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JOURNAL REFERENCE
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gill,S., Kolonay,J., Shetty,J., Tenover,F. and Weigel,L. Sequence of the Michigan vancomycin-resistant Staphylococcus aureus
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1 (bases 1 to 57889)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
2 (bases 1 to 57889)
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                                                                           complement (2317. .2802)
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                                                                                                                                                  complement (2317. .2802)
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                                                                                                   'locus_tag="VRA0004"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                locus_tag="VRA0003"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="similar to GP:13383313, and SP:P19380; identified y sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1/
transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="similar to GP:3676426, and GP:1041637; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene="repA"
                                                                                                                                                                                                                                                                                                                       transl_table
                                                                                                                                                                                                                                                                                                                                                                      imilarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    locus_tag="VRA0002" 179. .1853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein_id="AAQ17124.1"
db_xref="GI:33390918"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      product="replication initiator protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plasmid="pLW043"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .ocus_tag="VRA0001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocus_tag="VRA0001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .57889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEQDHRHIKVRKTRYQSINTAKNTLKGIECIYALYKKNRRSLQIYGFSPCHEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tag="VRA0002"
                                                                                                                                                                                                                                                                                                                       table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 table=11
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/codon_start=1
/transl_table=11
/product="TraA"
                                                                                                           /locus_tag="VRA0008"
/note="similar to GP:3676435, GB:X15505, GB:D45417, SP:P35030, and PID:37460; identified by
                                                                                                                                                                                                                             /locus_tag="VRA0008"
5057. .6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="G1:33390923"
/translation="MNYERYKQENKOVITVAVGYYLRYALSYRDISEILRGRGVNVHH
/translation="MNYERYKQENKKAYYKWRIDETYIKIKGKWSYLYRAIDAEGHTLDI
STVYRWVQBYAFILYQIWKKKHKAYYKWRIDETYIKIKGKWSYLYRAFKLKEDCHCTSK
                                                                                    sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DMTDFGHRSQQDPEFNEQYKEEMKKFKERI LNDDAFAKKYGNLGNVYGKQMRDMEDKN
GNHYDQLKSVIQQIKTNPNSRRHI VSAMNPTEI DSMALPPCHTMFQFYVQEGKLNCQL
YQRSADI FLGVPFNIASYALLTHLVAKECGLEVGEFIHTFGDAHI YSNHMDAIHTQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (2844. .3800)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RKTENSIGKELENRRNVVLTNQASFHHEGVDVINSLDEIKELSGHVFIFGGQTLYEAM
IDQVDDMYITVIDGKFQGDTFFPFYTFENWEVESSVEGQLDEKNTIFHTFLHLVRRKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mynpfDEAYHGLCEEILEIGNRRDDRTHTGTISKFGHQLRFDLT
KGFPLLTTKKVSFKLVATELL#FIKGDTNIQYLLKYNNNIWNEWAFENYVQSDDYHGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'trans] table=11

/product="thymidylate synthase"
/protein_id="AAQ17128.1"
/db_xref="GI:33390922"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (2844. .3800)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                locus_tag="VRA0007"
complement(4697. .4885)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      locus_tag="VRA0006"
note="similar to SP:P14506, and SP:P19380; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rdsylppqlkintdksifdinyedlelinyeshpaikapiav"
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note="similar to SP:P13954, and SP:P00469; identified by sequence similarity; putative"
                                                                                                                                                                                                   gene="traA"
                                                                                                                                                                                                                                                                                                                                                                                                      product="regulator of transfer gene ArtA"
protein_id="AAQ17130.1"
db_xref="GI:33390924"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LANLIEQDHRHIKVRKTRYQSINTAKNTLKGIECIYALYKKNRRSLQIYGFSPCHEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        locus_tag="VRA0005"
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                                                                                                                                                                                                                                                                                          gene="traA"
                                                                                                                                                                                                                                                                                                                                                                           translation="MNNNEENSVFFGKKKKKVSLHLLVDPDMKDEIIKYAQEKDFDNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transī
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              imilarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              locus_tag="VRA0007"
note="similar to GP:21623785; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="artA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="artA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       omplement (4697. .4885)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein_id="AAQ17129.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product="IS431mec transposase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           db_xref="GI:33390921"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=1
                                                                                                                                                                                                                                                                                                                                              AGREILKKGLEQIKSNK"
                                                                                                                                                                                                                                                                                                                       .6031
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protein_id="AAQ17131.1"

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                                                                                                                                            SOURCE
ORGANISM
                                                                                                                                                                                    VERSION
KEYWORDS
                                                                                                                                                                                                                             DEFINITION ACCESSION
                                                                                                                                                                                                                                                                                      OTPDVANA2
                                                                                                                                                                                                                                                                        Pocus
                                                                                                                                                                                                                                                                                                              RESULT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 20
    JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                         34820 TTCAGGCTCATCCTTCGGTG 34839
1 (bases 1 to 786)
Dutka-Malen,S., Molinas,C., Arthur,M. and Courvalin,P.
The VANA glycopeptide resistance protein is related to
D-alanyl-D-alanine ligase cell wall biosynthesis enzyme
Mol. Gen. Genet. 224 (3), 364-372 (1990)
                                                                                                                                            Oerskovia turbata
                                                                                                                                                                                                                                                OTPDVANA2
O.turbata Plasmid DNA for vancomycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
                                                                                                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Micrococcineae, Cellulomonadaceae; Oerskovia.
                                                                                                                                                                 Oerskovia turbata
                                                                                                                                                                                    vanA2 gene; vancomycin resistance
                                                                                                                                                                                                        X79049.1 GI:479085
                                                                                                                                                                                                                             X79049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                               TTCAGGCTCATCCTTCGGTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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EMYDDELFI YNSKNOALTNYDOLDEYHNROKOLOYNTKLEQERKORLTDTNKKYSENAK
EDLALSLGLTATALKGNINISNVEKVTDNESMVTIENEINGKSEHLISDEKDSFIEKA
KEKLTVSPSMRLGFEEFKNASGOIAMGFTEFFGARYDESTLENDPKVVATEKGYSVSV
FDKDGNKKDLTSADTFEEAVKLSKEMKHDNSLSRSEIELNQELEKKKI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MSVEQEVKDIMLDMLGEEKKVKENIIPRNVDASYKIFLNLNGKE
LAIVFVPFLLFLTIAFGVTFLMGLLNLITGFMVFIVGLIFGLTIYGLLTIRPISTKEN
IRMIDTIKOSQRFSRRQKVYFYKSKEGLGDDDV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /locus_tag="VRA0010"
/note="similar to GP:3676437; identified by sequence
similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /locus_tag="VRA0010"
6425. .6832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mikkfslttvyvaflsivlsnitigaenpgpkieqgiqQvQtpl
TGLIVAVGICAGVwivlkkklpgiddpmvknemprgvgmvlagvavgaalvwlvpwvyn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6048. .6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /locus_tag="VRA0011"
/note="similar to GP:3676438, and GP:3676438; identified
by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/transI_table=11
/product="TraC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="TraB"
/protein_id="AAQ17132.1"
/db_xref="GI:33390926"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /locus_tag="VRA0009"
/note="similar to GP:3676436; identified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene="traD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein_id="AAQ17133.1"
db_xref="GI:33390927"
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transl_table=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        locus_tag="VRA0011"
819. .7502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="traD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="traB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="traB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     locus_tag="VRA0009"
048. .6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 20; DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 57889;
                                                                                                                                                                                                                                                                        DNA
                                                                                                                                                                                                                                                    resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                        linear
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REFERENCE
                                                                                                              ORIGIN
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PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                        Query Match
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                               Local
     1 Similarity
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Location/Qualifiers
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Power, E.G.M.
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/protein id="CAA5651.1"
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/db xref="01:479086"
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/db xxef="InterPro:IPR010291"
/db xxef="InterPro:IPR011127"
/db xxef="InterPro:IPR01127"
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                                                                                                                                     /note="vanA equivalent
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                                                        Length 786;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Feb 21, 2002 this sequence version replaced gi:17384520. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is the entire insert of clone RP23-154F2 The true left end of clone RP23-183J6 is at 140238 in this sequence. The true right end of clone RP23-212F17 is at 93544 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from the RPCI-23 Mouse PAC Library

constructed by the group of Pieter de Jong.

For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISSPROT; Tr:,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers in the feature table with their source databases: Em:, EMBL; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30), an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Euarchontoglires; Glir
Sciurognathi; Muroidea; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VECTOR: pBACe3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-154F2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (16-FEB-2002) Wellcome Trust Sanger Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence was finished as follows unless otherwise noted: all
                                               /note="Tandem repeat. Forced join. Gap size be approximately 40bp by restriction digest
                                                                                                                                                                                                                                    /note="Sequence from overlapping clone RP11-212P17
(AL583890). Assembly confirmed by restriction digest.
12403. .12687
                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="3"
                                                                                                              note="Sequence from overlapping clone RP11-212F17 (AL583890). Assembly confirmed by restriction diges
                                                                                                                                                                                  note="Sequence from overlapping clone RP11-212F17 AL533890). Assembly confirmed by restriction digest."
                                                                                                                                                                                                                                                                                                                         clone_lib="RPCI-23"
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                                                                      note="Tandem repeat.
                                                                                                                                                                                                                                                                                                                                                       clone="RP23-154F2"
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Appl. Environ. Microbiol. 69 (9), 5609-5621 (2003)
2 (bases 1 to 801)
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                                                                        Elshahed, M.S., Senko, J.M., Najar, F.Z., Kenton, S.M., Roe, B.A., Dewers, T.A., Spear, J.R. and Krumholz, L.R.
                                                                                                         Bacteria; environmental samples.
1 (bases 1 to 801).
                                                                                                                                            uncultured bacterium
                                                     Bacterial diversity and sulfur cycling in a mesophilic sulfide-rich
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="16S ribosomal RNA"
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/country="Israel: Red
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mol_type="genomic DNA"
'isolation_source="coral mucus"
'specific_host="Fungia granulosa"
'db_xref="taxon:77133"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="RS.Muc.107"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="uncultured bacterium"
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                                                                                                                                                                                                    GI:32967957
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.0%; Score 18; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>,</u>
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Pred. No. 76;
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                                                                                                                                                                                                                                                        801 bp
ne ZB35
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1e RS.Muc.107
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94;
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Best Local S
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Submitted (20-JUN-2003) Botany and Microbiology, University of Submitted (20-JUN-2003) Botany and Microbiology, University of Oklahoma, 770 Van Vleet Oval, Norman, OK 73019, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Feldmannia irregularis virus a Feldmannia irregularis virus a Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; 1 (bases 1 to 48352)
Delaroque,N., Boland,W., Muller,D.G. and Knippers,R. Comparisons of two large phaeoviral genomes and evoluti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (24-JAN-2003) Bioorganics, Max Planck Institute for Chemical Ecology, Winzerlaer Strasse 10, Jena 07745, Germany Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Delaroque,N., Knippers,R., Mueller,D.G. and Boland,W.
Partial Nucleotide Sequence of the Feldmannia irregularis Virus
Firry-1 Genome: On the Evolution of Large Phaeoviral Genomes
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Feldmannia irregularis virus
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Delaroque,N., Knippers,R., Mueller,D.G. and Boland,W.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2003)
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                                                                                                                                                     /protein_id="AAR26876.1"
/db_xref="GI:38683700"
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/translation="MSTIKERRAVGKLKPLVPLHVKKERDAMRKLKEKKKQAKKEMQE
                                                                                                                                  complement (1349. .1768)
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|mol_type="genomic DNA"
|db_xref="taxon:77133"
                                                                                                                                                                                                                                                                                       /product="FirrV-1-B1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mol_type="genomic DNA"
/strain="FirrV-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 environmental_sample
                                                                                                    note="ORF B2"
                                                                                                                                                                                                                                                                                                                                                                                  note="similar to Ectocarpus siliculosus Virus-1 ORF 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                             'clone="contig B"
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protein_id="AAR26877.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.0%;
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Pred. No.
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97;
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g B, partial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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complement (5924...5986)
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VLFRYYDLFGAEREEKIARSKIVLNLHFWPESSLETHRIEYLLARGACVVSERSSDPV
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NCKYWAHDLATMSKEWYSARVAHUSFAVVGTM
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/note="ORF B5"
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                                                                    /note="ORF B8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLEEYRDKVDEELEKSQIYSRGRFGTYLYQISNQDHSVMQGVQVVDRILFGATETVLF
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HQYSLMLEVABSQYRKAPADLRTTCLAACRATNLTTASCRLVSBYHBRLBYGYPTPTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="Region:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (10706. .11050)
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SNLPALLEAYTDTVNRFMDLMLLANFFVAENSGMTGSIIYAGSKHSLHFEKYLAEMRY
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/note="ORF B11"
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PMTKGHSDTVEGGTGMGLAVARLLCRELGGDLVLTDQLTEGSTFHAFILLKCRSIVSW
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'db_xref="GI:38683712"
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db_xref="GI:38683711"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=
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| db_xref="GI:38683708"
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30817 TCAGGCTCATCCTTCAGTG 30799
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                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (24-AUG-2002) DOB Joint Genome Institute, 2) Drive, Walnut Creek, CA 94598, USA Draft Sequence Produced by DOB Joint Genome Institute www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                              Finishing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
www-shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 (bases 1 to 92474)
DOS Joint Genome Institute, Stanford Human Genome Center and
Alamos National Laboratory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 TCAGGCTCATCCTTCGGTG
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                                                                                                                                                                                                                                                                                                       NOTE: This is not the entire sequence of the clone (entire sequence is 163.3kb). It is clipped at the overlap with AC091489.
                                                                                                                                                                                                                                                                                                                                            Quality: Phrap Quality >=40 99.7% of Sequence;
Estimated Total Number of Errors is 0.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 92474)
DOB Joint Genome Institute, S
Alamos National Laboratories.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens chromosome 16 clone RP11-465L11, complete sequence AC131384
                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drive, Walnut Creek, CA 94598,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (21-AUG-2002) DOE Joint Genome Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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cc oligonucleotide composition comprising a first oligonucleotide comprising sequences substantially corresponding to nucleotides 870-896, 851-868 or 898-917 of the vanA gene, or its complement or portion, or an 898-917 of the vanA gene, or its complement or portion, or an collectide 387-404, 406-423 or 426-446 of the vanB gene, or its complement or portion, where the oligonucleotide hybridizes under comprising one or more oligonucleotide (s) specific for a vanA gene and/or vanB gene in a test sample, comprising the oligonucleotide mentioned compose. The method and kit are useful for detecting and/or amplifying genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying control of food, water, pharmaceutical proposes, such as for quality control of food, water, pharmaceutical products or other products requiring microbiological control. The present sequence represents a probe for Enteropoccus faecium vanA, which is used in an example from the
Sequence 27 BP; 3 A; 8 C; 6 G; 10 T; 0 U; 0 Other;
                                                                                                                               present invention.
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Query Match
Best Local 9
Matches
27;
       Similarity
Conservative
      100.0%;
0
      Score 27;
Pred. No.
Mismatches
      DB 14;
0
             Length
             27;
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Gaps
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밁 Ś AAH02300; AAH02300 standard; DNA; 1032 BP

Species specific; genus specific; family specific; probe; detection; identification; algal; archaeal; bacterial; fungal; parasitical; microorganism; diagnosis; translation elongation factor Tu; toxin; translation elongation factor G; RecA recombinase; resistance; catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine; primer; ds. Enterococcus faecium nucleotide sequence SEQ 24-JUL-2001 (first entry) ID NO: 2293

Enterococcus faecium.

WO200123604-A2

05-APR-2001

28-SEP-2000; 2000WO-CA001150.

28-SEP-1999; 19-MAY-2000; 99CA-02283458. 2000CA-02307010.

(INFE-) INFECTIO DIAGNOSTIC (IDI) INC.

Picard ₽J, ลี Roy Boissinot M, PH; Huletsky A, Menard ú Ouellette

Z

WPI; 2001-245006/25

Nucleic acid sequences are used to generate universal probes and which can be used to identify and detect the presence of algal, bacterial, fungal and parasitical species in a test sample. and archaeal,

Disclosure; Page 1578; 1580pp; English.

The invention relates to a method for detecting vancomycin resistance gene vanA and/or vanB nucleic acid molecules in a sample comprising contacting the sample with a vanA- and/or vanB-specific oligonucleotide probe or primer, and detecting or determining the presence or amount of hybrid formation or amplified nucleic acid. Also described: (1) an

Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-and/or vanB-specific oligonuclectide probes or primers.

SEQ ID NO 3; 33pp; English.

WPI; 2005-222218/23.

The present invention describes a method for generating a repertory of nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nuclei nucleic

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         competitive inducer sequestration; vanH promoter; vanR gene product; Enterococcus; Staphylococcus; Streptococcus; Gram-positive bacterium; antibiotic susceptibility; ex vivo eradication; in vivo eradication;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-AUG-2000; 2000WO-US022086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved. AAH00010 to AAH002304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200112803-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glycopeptide resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vancomycin resistance reduction; antisense expression inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterococcus faecium vanA gene, SEQ ID NO:21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF76039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF76039 standard; DNA; 1032 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1032 BP; 303 A; 197 C; 264 G; 268 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCTATCCTGTTTTTGTTAAGCCGGCGC 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTATCCTGTTTTTGTTAAGCCGGCGC 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleotide sequences and primers/probes which are given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                y; ex vivo eradication; in vivo eradication;
VanA gene cluster; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             archaeal, bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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introducing a antisense vancomycin-resistance ge

gene

expression,

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enhancing

vanH

promoter

Roy

PH;

Inouye RT,

Torres-Viera C,

Moellering R,

Gold H,

Eliopoulos

17-AUG-1999;

99US-0149313P

(ВЕТН-) ВЕТН

ISRAEL DEACONESS MEDICAL CENT

Example; Page 52; 59pp; English

Reducing vancomycin-resistance in vancomycin-resistant organism b introducing a antisense vancomycin-resistance molecule to inhibit

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Matches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in glycopeptide resistant enterococci. The methods of the invention are useful for reducing vancomycin resistance in a vancomycin resistant organism, particularly Enterococcus faecium and Enterococcus faecalis, but also in other Gram-positive bacteria such as Staphylococcus sp. and Streptococcus sp., to which Enterococcus faecium and Enterococcus faecalis have the potential to transfer resistance determinants. The antisense molecules are useful in the treatment of infection and colonisation by vancomycin resistant enterococci and other clinically colonisation by vancomycin resistant enterococci and other clinically
                Bergeron MG,
Picard FJ,
                                                                                                                                                                                                                                                                                                                                                                 identification; algal; archaeal; bacterial; fungal; parasitical; microorganism; diagnosis; translation elongation factor Tu; toxin; translation elongation factor G: RecA recombinase; resistance; catalytic subunit of proton-translocating ATPase; antimicrobial; v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   humans; and in primary or adjuvant therapy for vancomycin-resistant enterococcal infections. The gene based strategy targets key vancomycin resistance determinants and results in restoration of vancomycin susceptibility in previously glycopeptide- resistant enterococci. Sequences AAP67036-AAP67042 represent genes of the Enterococcus faecium
                                                                                                                                                                             28-SEP-2000; 2000WO-CA001150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        significant pathogens, and may be used for the ex vivo eradication of vancomycin-resistant enterococci from frequently colonised settings, such as intensive care units, haemodialysis units, and chronic care facilities; for the in vivo clearance of vancomycin-resistant enterococci from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vancomycin resistance gene antisense nucleic acid into the organism, antisense oligonucleotides complementary to AAP76023-AAP76031 are particularly preferred for this purpose. The second method involves providing additional vanH promoter sequences which are not operatively
                                                                                                                  28-SEP-1999; 99CA-02283458
19-MAY-2000; 2000CA-02307010
                                                                                                                                                                                                                         05-APR-2001.
                                                                                                                                                                                                                                                               WO200123604-A2
                                                                                                                                                                                                                                                                                                    Enterococcus gallinarum
                                                                                                                                                                                                                                                                                                                                                primer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterococcus gallinarum nucleotide sequence SEQ ID NO:1055.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH01064 standard; DNA; 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1032 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coupled to a vancomycin resistance gene, so that the phosphorylated vank gene product (which induces vanH promoter activity) is competitively
                                                                           (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH01064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       colonised gastrointestinal or genitourinary tracts of animals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequestered.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vancomycin-resistant organism. One method involves introducing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to methods of reducing vancomycin resistance in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27;
                                                                                                                                                                                                                                                                                                                                                                                                                         specific; genus specific; family specific; probe; ication; algal; archaeal; bacterial; fungal; paras;
                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Both methods are able to restore antibiotic susceptibility ide resistant enterococci. The methods of the invention are
                                   Boissinot M, Huletsky A,
                                                                                                                                                                                                                                                                                                                                                               of proton-translocating ATPase; antimicrobial; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       303 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 27;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         268 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.03;
                                   Menard
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                                   Ouellette
                                                                                                                                                                                                                                                                                                                                                                                                                                                detection;
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Which ca

ic acid sequences are used to generate universal probes and primers can be used to identify and detect the presence of algal, archaeal, rial, fungal and parasitical species in a test sample.

2001-245006/25

bacterial,

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cc nucleic acids of tuf, fus, atpD and/or reck genes from which probes cc and/or primers are derived. The method comprises amplifying the nucleic cacids of determined algal, archaeal, bacterial, fungal and parasitical cc species with a combination of defined primer pairs. The method can be cc used for producing probes and/or primers for detecting one or more cc related microorganisms e.g. algae, archaea, bacteria, fungi and cc parasitics, for universal detection and for specific and ubiquitous cc detection and identification of an algal, archaeal, bacterial, fungal and cc parasitics from the invention can be used for the universal detection of any bacterial, fungal and cc using the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the detection of cc at least one antimicrobial agent resistance gene or at least one toxin cg ene. hexa nucleic acids are used for the specific and ubiquitous cc detection and for identification of Streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against cc used to design a therapeutic agent which is effective against cc used to design a therapeutic agent which is effective against cc which can be detected include Abhotrophia adiacens, Bordetella sp., cc corynebacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria cc gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster cc an hour and improved accuracy is also achieved. Ahhoolo to Ahhoolo cc exemplification of the present invention
ARBSULT 5
AAHO10A
AAHO10A
AC AAHO
AC A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                               Species specific; genus specific; family specific; probe; detection; identification; algal; archaeal; bacterial; fungal; parasitical; microorganism; diagnosis; translation elongation factor Tu; toxin; translation elongation factor G; RecA recombinase; resistance;
                                                                                                                                                                                                                                                                                                                                                                                         primer; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1218 BP; 364 A;
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                                 28-SEP-1999;
19-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH01063
                                                                                                                           28-SEP-2000; 2000WO-CA001150.
                                                                                                                                                                                                                                                          WO200123604-A2
                                                                                                                                                                                                                                                                                                                          Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTATCCTGTTTTTGTTAAGCCGGCGC 27
                                                                                                                                                                                                                                                                                                                                                                                                                    subunit of proton-translocating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                 99CA-02283458
2000CA-02307010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleotide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 27; DB 4;
Pred. No. 0.031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a method for generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       ATPase; antimicrobial; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO:1054.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0 Other;
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The present invention describes a method for generating a repertory of CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes CC and/or primers are derived. The method comprises amplifying the nucleic CC acids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be CC used for producing probes and/or primers for detecting one or more CC used microorganisms e.g. algae, archaea, bacteria, fungi and can be combinated in the combination of an algal, archaeal, bacterial, fungal and combinations of an algal, archaeal, bacterial, fungal and combinations are genes, family and group. A nucleic acid (I) obtained CC using the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the detection of any bacterium, fungus or parasite in a sample and for the detection of at least one antimicrobial sgent resistance gene or at least one toxin combinated to design a therapeutic agent which is effective against which to design a therapeutic agent which is effective against which to design a therapeutic agent which is effective against which is effective against gp. . Using DNA based tests provides faster CC corynebacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria gonorrhoeae and Staphylococcus sp. . using DNA based tests provides faster cresults than substrate specificity tests as results can be determined in a hour and improved accuracy is also achieved. AAH00010 to AAH002304 represent nucleotide sequences and primers probes which are given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal, bacterial, fungal and parasitical species in a test sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 27; Page 1001; 1580pp; English.
                                               exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-245006/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roy PH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Σ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Huletsky
                                                  invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ۶
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Query Match Best Local 27; Similarity CCTATCCTGTTTTTGTTAAGCCGGCGC 27 Conservative 100.0%; 100.0%; 0 Score 27; Pred. No. Mismatches 0.031; DB 4; 0 Length 1232; Indels 0 Gaps

0

Sequence 1232 BP; 367 A; 228 C; 313 G; 323 T; 0 U; 1 Other;

RESULT 6

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578 \vdash

CCTATCCTGTTTTTGTTAAGCCGGCGC 604

S

AAH01061 standard; DNA; 1237

24-JUL-2001 (first entry)

Enterococcus faecium nucleotide sequence SEQ ID NO:1052

Species specific; genus specific; family specific; probe; detection; identification; algal; archaeal; bacterial; fungal; parasitical; microorganism; diagnosis; translation elongation factor Tu; toxin; translation elongation factor G; RecA recombinase; resistance; catalytic subunit of proton-translocating ATPase; antimicrobial; vac primer; de. antimicrobial; vaccine;

Enterococcus faecium

WO200123604-A2

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AAHO1058
ID AAHO
XX
AC AAHC
XX
AC AAHC
XX
AC AAHC
XX
Brite
XX
Brite
XX
XX
Spec
XW
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XW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC related microorganisms e.g. algae, archaea, bacteria, fungi and comparables, for universal detection and for specific and ubiquitous contection and identification of an algal, archaeal, bacterial, fungal and corporatives genus, family and group. A nucleic acid (I) obtained content of any bacterium, fungus or parasite in a sample and for the detection of any bacterium, fungus or parasite in a sample and for the detection of content of any bacterium, fungus or parasite in a sample and for the detection of content of any bacterium, fungus or parasite in a sample and for the detection of content of streptococcus pneumoniae. (I) can be content of content of streptococcus pneumoniae. (I) can be content of detection and for identification of Streptococcus pneumoniae. (I) can be content of design a therapeutic agent which is effective against content of microorganisms. Microbial species or genus or family or phylum or group content of the detection sp., Enterobacteriaceae group, Streptococcus sp., Neisseria converted in the converted and Staphylococcus sp. Using DNA based tests provides faster converses than substrate specificity tests as results can be determined in converses than substrate specificity tests as results can be determined in converses than substrate specificity tests as results can be determined in converses than substrate specificity tests as results can be determined in converses than substrate specificity tests as results can be determined in converses than substrate specificity tests as results can be determined in converses than substrate specificity tests as results can be determined in converses than substrate specificity tests as results can be determined in converses than substrate specificity tests.
                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
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acids of determined algal, archaeal, bacterial, rungar and primer pairs. The method can species with a combination of defined primer pairs. The method can used for producing probes and/or primers for detecting one or more used for producing probes and/or primers for detecting one or more used for producing probes and/or primers for detecting fungiants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a method for generating a repettory of nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bergeron N
Picard FJ,
                                                                        catalytic
                                                                                               identification; algal; archaeal; bacterial; fungal; parasitical; microorganism; diagnosis; translation elongation factor Tu; toxin; translation elongation factor G; RecA recombinase; resistance;
                                                                                                                                                                          Species specific; genus specific; family specific; probe; detection
                                                                                                                                                                                                                            Enterococcus
                                                                                                                                                                                                                                                                             24-JUL-2001
                                                                                                                                                                                                                                                                                                                              AAH01058
                                                                                                                                                                                                                                                                                                                                                                          AAH01058 standard; DNA; 1241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1237 BP; 366 A; 235 C; 314 G; 322 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27; Page 999; 1580pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bacterial,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTATCCTGTTTTTGTTAAGCCGGCGC 27
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                                                                           subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fungal and parasitical species
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences are used to generate universal probes and primers used to identify and detect the presence of algal, archaeal, ungal and parasitical species in a test sample.
                                                                                                                                                                                                                         faecium nucleotide sequence SEQ ID NO:1049
                                                                                                                                                                                                                                                                          (first entry)
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                                                                           유
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                                                                           proton-translocating ATPase; antimicrobial; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .0%; Score 27; DB 4; .0%; Pred. No. 0.031; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
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Enterococcus faecium

RESULT 8
AAHO1059
ID AAHO
XX AAHO
AC AAHO
XX AAHO
XX Ente
XX XX
DE Ente
XX XX Ente
XX

(first entry)

standard, DNA, 1249 BP

Enterococcus 24-JUL-2001

Species specific; genus specific; family specific; probe; detection; identification; algal; archaeal; bacterial; fungal; parasitical; microorganism; diagnosis; translation elongation factor Tu; toxin;

gallinarum nucleotide sequence SEQ ID NO:1050.

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561

CCTATCCTGTTTTTGTTAAGCCGGCGC 27

CCTATCCTGTTTTTGTTAAGCCGGCGC 587

Matches.

27;

Conservative

0

Indels

0

Gaps

0

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cc species with a combination of defined primer pairs. The method can be cused for producing probes and/or primers for detecting one or more cc related microorganisms e.g. algae, archaea, bacteria, fungi and cetection and identification of an algae, archaea, bacteria, fungi and cc parasites, for universal detection and for specific and ubiquitous cd etection and identification of an algal, archaeal, bacterial, fungal and comparasite in a sample and for the universal detection cf any bacterium, fungus or parasite in a sample and for the detection of at least one antimicrobial agent resistance gene or at least one toxin cc detection and for identification of streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against cused to design a therapeutic agent which is effective against complete and be detection be cused to design a therapeutic agent which is effective against cc which can be detected include Abiotrophia adiacens, Bordetella sp., cc wycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria comportioeae and staphylococcus sp. Using DNA based tests provides faster cresults than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved. AAH00010 to AAH002304 crepresent nucleotide sequences and primers/probes which are given in the
                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal bacterial, fungal and parasitical species in a test sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-245006/25
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19-MAY-2000; 2000CA-02307010
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                                                                                                                                                      Sequence 1241 BP; 371 A; 228 C; 317 G; 325 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present inven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; Page 997; 1580pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bergeron MG,
                                                                                                                                                                                                                                  exemplification of the present invention
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                                       Local
                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention describes a method for generating a repertory ds of tuf, fus, atpD and/or recA genes from which probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roy PH;
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                                           100.0%;
.0%; Score 27; D
.0%; Pred. No. 0.
0; Mismatches
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                                               0.031;
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                                                                                   DB
                                                                               4; Length 1241;
                                                                                                                                                          U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouellette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         archaeal,
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RESULT 9
AAH01062
ID AAH0
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AC AAH0
XX
AC AAH0
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AC AAH0
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                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a method for generating a repertory of concleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic concids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be considered microorganisms e.g. algae, archaea, bacteria, fungia and parasitical grassites, for universal detection and for specific and ubiquitous concentration and identification of an algal, archaeal, bacterial, fungal and grassitical species, genus, family and group. A nuclaic acid (1) obtained concentration and interest for detection of any bacterial, fungal and concentration of any bacterial, fungal and grassitical species, genus, family and group. A nuclaic acid (1) obtained concentration, fungus or parasite in a sample and for the detection of any bacterium, fungus or parasite in a sample and for the detection of any bacterium, fungus or parasite in a sample and for the detection of at least one antimicrobial sgent resistance gene or at least one toxin gene. hexA nucleic acids are used for the specific and ubiquitous concentration and for identification of streptcococcus pneumoniae. (1) can be used to design a therapeutic agent which is effective against concentration of include Abiotrophia adiacens, Bordetella sp., complete than substrate specificity tests as results can be determined in the createst substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved. AAH00010 to AAH002304 creates and primers/probes which are given in the
                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal bacterial, fungal and parasitical species in a test sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 27; Page 998; 1580pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation elongation factor G; RecA recombinase; resistance; catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
                      24-JUL-2001
                                                                                               AAH01062 standard;
                                                                                                                                                                                                                                                                                                                                                    Sequence 1249 BP; 373 A; 235 C; 316 G; 325 T; 0 U; 0 Other;
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                                                            AAH01062;
                                                                                                                                                                                                                                                                                                                                                                                           exemplification of the present invention
                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                590
                                                                                                                                                                                                                                                                         l Similarity
27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 de.
                                                                                                                                                                                                                   CCTATCCTGTTTTTGTTAAGCCGGCGC 27
                                                                                                                                                                                              CCTATCCTGTTTTTGTTAAGCCGGCGC 616
                                                                                                                                                                                                                                                                           Conservative
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                  (first entry)
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                                                                                               DNA; 1263
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                                                                                                                                                                                                                                                                     Score 27; DB 4;
Pred. No. 0.031;
, Mismatches 0
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Species specific; genus specific; family specific; probe; detection; identification; algal, archaeal, bacterial, fungal, parasitical; microorganism; disagnosis; translation elongation factor Tu; toxin; translation elongation factor G; RecA recombinase; resistance; catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
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19-MAY-2000; 2000CA-02307010.
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Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal bacterial, fungal and parasitical species in a test sample.

Page 1000; 1580pp; English

The present invention describes a method for generating a repertory of nucleic acids of tuf, fus, atpD and/or recA genes from which probes cand/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical consected microorganisms e.g. algae, archaea, bacterial, fungal and parasitical consected microorganisms e.g. algae, archaea, bacterial, fungal and can be related microorganisms e.g. algae, archaea, bacterial, fungal and can be detection and identification of an algal, archaeal, bacterial, fungal and comparasitical species, genus, family and group. A nucleic acid (I) obtained comparasitical species, genus, family and group. A nucleic acid (I) obtained comparasitical species, genus, family and group. A nucleic acid (I) obtained comparasitical agent resistance gene or at least one toxin gene. hexA nucleic acids are used for the specific and ubiquitous of any bacterium, fungus or parasite in a sample and for the detection of detection and for identification of streptococcus pneumoniae. (I) can be used to design a therapeutic agent resistance gene or at least one toxin comparasity. Pseudomonads group, Escherichia coli, which can be detected include Abiotrophia adiacens, Bordeteila sp., (C corynebacteriaceae family, Pseudomonads group, Escherichia coli, which can be detected include Abiotrophia adiacens, Bordeteila sp., (Pseudomonads group, Escherichia coli, Pseudomonads group, Escherichia coli, can be determined in an also achieved. AAH002304 crepresent nucleotide sequences and primers/probes which are given in the exemplification of the present invention

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Sequence
 1263
BP; 378
A; 234 C; 321 G; 330 T; 0 U; 0 Other;
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밁 δ Matches Query Match Best Local Similarity 27; μ CCTATCCTGTTTTTGTTAAGCCGGCGC 27 CCTATCCTGTTTTTGTTAAGCCGGCGC 608 Conservative 100.0%; Score 27; 100.0%; Pred. No. 0 Mismatches 0.031; DB 4; 0 Length 1263; Indels 0 Gaps

0

RESULT 10 AAH01065 ID AAH01

AAH01065 standard; DNA; 1265 **B**P

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문
                    8
  592
                     CCTATCCTGTTTTTGTTAAGCCGGCGC 27
 CCTATCCTGTTTTTGTTAAGCCGGCGC
618
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Best Local Similarity

100.0%;

Score Pred.

No.

DB 4;

Length 1269

Query Match

Sequence 1269

BP;

380 A; 238 C; 321 G; 330 T; 0 U; 0 Other;

Best Matches Query Match related microorganisms e.g. algae, archaea, bacteria, fungi and parasites, for universal detection and for specific and ubiquitous detection and identification of an algal, archaeal, bacterial, fungal and parasitical species, genus, family and group. A nucleic acid (I) obtained using the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the detection of at least one antimicrobial agent resistance gene or at least one toxin gene. hexa nucleic acids are used for the specific and ubiquitous detection and for identification of Streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against Corynebacterium sp., Enterobacteriaceae group, Escherichia coli, Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved. AAH00010 to AAH002304 represent nucleotide sequences and primers/probes which are given in the exemplification of the present invention used to design a therapeutic agent which is effective against microorganisms. Microbial species or genus or family or phylum or group which can be detected include Abiotrophia adiacens, Bordetella sp., species with a combination of defined primer pairs. The method can used for producing probes and/or primers for detecting one or more related microorganisms e.g. algae, archaea, bacteria, fungi and The present invention describes a method for generating a repertory of nucleic acids of tuf, fus, atpb and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal bacterial, fungal and parasitical species in a test sample. Sequence 1265 Claim Bergeron MG, Picard 28-SEP-1999; 99CA-02283458. 19-MAY-2000; 2000CA-02307010. 28-SEP-2000; 2000WO-CA001150. 05-APR-2001. dentification; algal; archaeal; bacterial; fungal; parasitical; microorganism; diagnosis; translation elongation factor Tu; toxin; translation elongation factor G; RecA recombinase; resistance; catalytic anhunit of protoportion factor G; RecA recombinase; resistance; (INFE-) INFECTIO DIAGNOSTIC (IDI) WO200123604-A2 Enterococcus faecium catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine; Species specific; Enterococcus 24-JUL-2001 AAH01065; dentification; Local 27; Page 1002; 1580pp; English. ĘJ, Similarity Roy Conservative faecium nucleotide sequence SEQ ID NO:1056 B₽; (first entry) Boissinot M, PH; 379 A; 237 C; 320 G; 329 T; 0 U; 0 Other; genus specific; family specific; probe; lgal; archaeal; bacterial; fungal; parasi 100.0%; <u>.</u> Huletsky A, Score 27; Pred. No. (Mismatches bacterial, fungal and 0.031; Menard C, DB 4; 0; Length 1265; Indels Ouellette detection; 0 Gaps þe 0

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The present invention describes a method for generating a repertory of CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes CC and/or primers are derived. The method comprises amplifying the nucleic CC acids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be CC used for producing probes and/or primers for detecting one or more CC related microorganisms e.g. algae, archaea, bacteria, fungi and CC parasitical species, genus, family and group. A nucleic acid (I) obtained CC quartical to genus, family and group. A nucleic acid (I) obtained CC quartical the method of the invention can be used for the universal detection of at least one antimicrobial agent resistance gene or at least one toxin CC at least one antimicrobial agent resistance gene or at least one toxin CC quartical acid include abiotrophia adiacens, bacterive against microorganisms. Microbial species or genus or family or phylum or group which can be detected include Abiotrophia adiacens, Bordetella sp., CC crynebacterium sp., Enterobacteriaceae group, Escherichia coli Mycobacteriaceae family, Pseudomonade group, Streptococcus sp., Neisseria CC an hour and taphylococcus sp. Using DNA based tests provides faster results than substrate specificity tests as results can be determined in the contract of the semences and orients/probe which are civen in the
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exemplification
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sequences and primers/probes which are
he present invention
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                   CC species with a combination of defined primers pairs. The method can be considered microorganisms e.g. algae, archaea, bacteria, fungi and combination for universal detection and for specific and ubiquitous content of the inversal detection and for specific and ubiquitous content of the inversal detection and group. A nucleic acid (I) obtained consists of the invention can be used for the universal detection of an algal, archaeal, bacterial, fungal and content of any bacterium, fungus or parasite in a sample and for the detection of content of any bacterium, fungus or parasite in a sample and for the detection of content of any bacterium, fungus or parasite in a sample and for the detection of content of any bacterium, fungus or parasite in a sample and for the detection of content of any bacterium, fungus or parasite in a sample and for the detection of content of any bacterium of the specific and ubiquitous content of any bacterium and for identification of Streptococcus spreamoniae. (I) can be used to design a therapeutic agent which is effective against confidence of any bacterium sp., Enterobacteriaceae group, Escherichia coli, con be confident of the proposed course of the specific and ubiquitous courses. (I) can be confident of the proposed course sp., Neisseria confidence and Staphylococcus sp., Neisseria confidence and Staphylococcus sp., Using DNA based tests provides faster confidence and improved accuracy is also achieved. AAH00010 to AAH002304 confidence and course of the proposed course which are given in the combination of the course of the proposed course of the pr
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   related microorganisms e.g. algae, archaea, bacteria, fungi and parasites, for universal detection and for specific and ubiquitous detection and identification of an algal, archaeal, bacterial, fungal and parasitical species, genus, family and group. A nucleic acid (I) obtained using the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the detection of at least one antimicrobial agent resistance gene or at least one toxin gene. hexh nucleic acids are used for the specific and ubiquitous detection and for identification of Streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against microorganisms. Microbial species or genus or family or phylum or group which can be detected include Abiotrophia adiacens, Bordetella sp., Corynebacterium sp., Enterobacteriaceae group, Escherichia coli, Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    microorganism; diagnosis; translation elongation factor Tu; toxi translation elongation factor G, RecA recombinase; resistance; catalytic subunit of profon-franchionaria-
                                                                                                                                                                                                                                      The present invention describes a method for generating a repertory of nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more related microorganisms e.g. algae, archaea, bacteria, fungi and
                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal, bacterial, fungal and parasitical species in a test sample.
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19-MAY-2000; 2000CA-02307010.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterococcus faecium nucleotide sequence SEQ ID NO:1139.
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ilarity 100.0%;
Conservative 0;
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algal; archaeal; bacterial;
I include and a group, Eschelleriaceae group, Eschelleriaceae group, Streptococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Huletsky A,
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                                          comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes and a donor fluorescent group and a corresponding fluorescent group. The method is useful for detecting the presence or absence of vancomycin-resistant enterococci in a biological sample, e.g. stool samples, anal or perirectal swabs, blood and body fluids from an individual. The method replaces standard culture methods and reduces the cost. The method provides rapid vancomycin resistant enterococcus real time PCR assay which is useful for beginning the antimicrobial therapy immediately to treat hospital acquired infection. The present sequence is an
                                                                                                                                                                                                   The invention relates to detecting the presence or absence of vancomycin-
resistant enterococci (VRE) in a sample, comprising performing a cycling
step by amplifying a sample with pair of vanA or vanB primers and
hybridising the sample with a pair of vanA or vanB probes, labelled with
donor and acceptor fluorescent group, respectively, detecting
fluorescence resonance energy transfer (FRET), where the presence of FRET
indicates presence of VRE. Also included is an article of manufacture,
respectively.
                                                                                                                                                                                                                                                                                                                                                                                                            Detecting presence or absence of vancomycin-resistant enterococci in biological sample from individual comprises using real time polymera
                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 10; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cockerill FR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
                      oligonuclectide comprising sequences substantially corresponding to nuclectides 387-404, 406-423 or 426-446 of the vanB gene, or its complement or portion, where the oligonuclectide hybridizes under stringent hybridization conditions to vanh or vanB DNA; and (2) a kit comprising one or more oligonuclectide(s) specific for a vanA gene and/or vanB gene in a test sample, comprising the oligonuclectide mentioned above. The method and kit are useful for detecting and/or amplifying genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying antibiotic resistance genes (e.g. vancomycin-resistant enterococcus). They may also be used in other industrial purposes, such as for quality control of food, water, pharmaceutical products or other products an equiring microbiological control. The present sequence represents an Enterococcus faecium vanA nucleotide sequence from the present invention.
                                                                                                                                                                                                                                                                  oligonucleotide composition comprising a first oligonucleotide comprising sequences substantially corresponding to nucleotides 870-896, 851-868 or 898-917 of the vanA gene, or its complement or portion, or an
                                                                                                                                                                                                                                                                                                                                             The invention relates to a method for detecting vancomycin resistance gene vanA and/or vanB nucleic acid molecules in a sample comprising contacting the sample with a vanA- and/or vanB-specific oligonucleotide probe or primer, and detecting or determining the presence or amount of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e.g. identifying vancomycin-resistant.enterococcus, com and/or vanB-specific oligonucleotide probes or primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2005-222218/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA detection; antibiotic-resistance; vancomycin; vanA; gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; SEQ ID NO 1; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-SEP-2003; 2003US-00661094.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2005058985-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterococcus faecium vanA DNA sequence SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADY59927 standard; DNA; 1768
                                                                                                                                                                                                                                                                                                                                  hybrid formation or amplified nucleic acid. Also described:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-SEP-2003; 2003US-00661094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-MAR-2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DODG/) DODGSON K J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          870 CCTATCCTGTTTTTGTTAAGCCGGCGC 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTATCCTGTTTTTGTTAAGCCGGCGC 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 27; DB 12
Pred. No. 0.033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comprises using vanA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                  (1) an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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Query Match Best Local 9 Matches

Similarity

100.0%; Score 27; 100.0%; Pred. No.

Conservative

<u>.</u>

Mismatches

<u>,,</u>

0;

Gaps

0

0.033; DB 14;

Length 1768; Indels

Sequence 1768 BP; 537 A; 336 C; 437 G; 458 T; 0 U; 0 Other;

Sequence

1768

537

A; 336 C;

437

<u>۾</u>

458 T; 0 U; 0 Other;

vanA, B₽;

vancomycin resistance gene.

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RESULT 16
AAT28569
ID AAT286
XX AAT28
XX Detector
XW Esche
XW Infec
XW Infec
XX Infe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemophilus influenzae; Moraxella catarrhalis; septic: infection; intra-abdominal infection; skin infection; bacterial resistance; beta-lactam antition:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proteus mirabilis; Streptococcus pneumoniae; Staphylococcus aureus; Staphylococcus epidermidis; Enterococcus faecalis; respiratory tract; Staphylococcus saprophyticus; Streptococcus pyogenes; urinary tract;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detection; probe; amplification primer; bacterial pathogen; pneu
Escherichia coli; Klebsiella pneumoniae; Pseudomonas aeruginosa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT28569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9608582-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacterial antibiotic resitance gene, vanH, vanA and vanX, probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT28569 standard; DNA; 2607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTATCCTGTTTTTGTTAAGCCGGCGC 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             septicaemia; meningitis;
```

pneumonia;

밁 8

21-MAR-1996. (BERG/) BERGERON M G. (OUEL/) OUELLETTE M. (ROYP/) ROY P H. 12-SEP-1995; 94US-00304732. 95WO-CA000528.

Bergeron MG,

Ouellette

Z,

Roy

PH

Method for the detection of bacterial species using probes and primers allows detection and quantification of antibiotic resistant bacteria in patients, the environment and

Claim 94; Page 145-147; 216pp; English.

CC sample. The method of the invention comprises using probes and/or comprises. The method of the invention comprises using probes and/or amplification primers which are specific, ubiquitous and sensitive for comprises and the presence and/or amount of nucleic acids from selected bacterial species in any sample, where the bacterial nucleic acid comprises a selected target region hybridisable with the probes or comprises. The method comprises contacting the sample with the probes or comprises and detecting the presence and/or amount of hybridised primers or complification products as and indication of the presence and/or amount of the bacterial species. This method may be used to detect commonly concuntered bacterial pathogens, e.g. Escherichia coli, Klebsiella compensoriae, Pseudomonas aeruginosa, Proteus mirabilis, Streptococcus preumoniae, Staphylococcus aureus, Staphylococcus epidermidis, compresence, Haemophilus influenzae and Moraxella catarrahais. These bacterial species are associated with approx. 90% of urinary tract conculting septicaemia, meningitis, pneumonia, intra-abdominal infections, and other severe respiratory tract infections. The method control also be used to evaluate a bacterial resistance to beta-lactam The sequences given in AAT28560-76 represent fragments derived is bacterial antibiotic resistance genes which were used as probes method of the invention for the detection of bacterial species is may also be used antibiotics in a ín the

Sequence 2607 BP; 768 ? 506 ü 652 ဂ္ 681 ij 0 ₽ 0 Other

Matches Query Match Best Local

l Similarity 27; Conserv

100.0%; ilarity 100.0%; Conservative 0

0

Pred. No. 0.0 ; Mismatches Score 27;

0.035; DB 4;

Length 2607

Indels

0,

Gaps

0

Sequence 2607

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ABA76994
XX ABA7
XX AB
                                                                                  The invention relates to detecting target bacterial species suspected to be present in a sample, comprising contacting nucleic acids of target bacterial species with an amplification primer pair derived from a context of the target bacterial DNA fragment (ABA76825-ABA76861) specific for the target bacterial species but ubiquitous for different strains, amplifying the currents are indication of the presence or amount of an amplified context of the target bacterial species. The invention includes primers and probes (ABA76862-CC ABA76894) against the target bacterial species, especially E.coli, CC E.pneumoniae, P.acruginosa, P.mirabilis, S.pneumoniae, S.aureus, CC S.epidermidis, E.faecalis, S.saprophyticus, S.pyogenes, H.influenzae, C. M.catarrhalis and/or group A Streptococci producing exotoxin A gene species. A, suspected to be present in a sample which is obtained from human cc patients, animals, environment or food, and which consists of one or more bacterial colonies. Oligonucleotide probes and primers complementary to the bacterial genes encoding resistance to antibiotics such as bla (tem), bla(shv), aadB, sacCl, sacCl, sacCl, sacA4, mecA, vanA, vanH, covanX, satA, sacA-aphb, vat, vas, msrA, sul and/or int (ABA75985-ABA77001) care also useful to identify commonly encountered and clinically important resistance genes. The invention provides a rapid method of bacterial colentification that can be achieved, which reduces the time currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Method for detecting target bacterial species in a sample, detecting the presence or amount of bacterial nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-615034/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detection; antibiotic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 16; Page 160-162; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer derived from bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bergeron MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTATCCTGTTTTTGTTAAGCCGGCGC 1481
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                                                                 for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bacterial species; animal; food; environment; resistance; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  resistance detection polynucleotide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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   BP; 768 A; 506 C; 652 G; 681 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouellette M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95NZ-00501596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95NZ-00501596
                                                              identification of pathogens in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
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Pred. No. 0.035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA, specific for the target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                     the clinical laboratory
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amplified
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Sequence 3946 BP; 1235 A; 706 C; 936 G; 1069 T; 0 U; 0 Other;

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                                       which can be detected include ALAURIUM, Escherichia coli, Corynebacterium sp., Enterobacteriaceae group, Escherichia coli, Wycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved. AAH00010 to AAH002304 represent nucleotide sequences and primers/probes which are given in the
                                                                                                                                                                                                                                                                                                          detection and identification of an algal, archaeal, bacterial, fungal and parasitical species, genus, family and group. A nucleic acid (I) obtained using the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the detection of at least one antimicrobial agent resistance gene or at least one toxin gene. hava nucleic acids are used for the specific and ubiquitous detection and for identification of Streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and/or primers and loss primer pairs. The method can species with a combination of defined primer pairs. The method can used for producing probes and/or primers for detecting one or more used for producing probes and/or primers for detecting and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be
             represent nucleotide sequences and primers/probes which are exemplification of the present invention
                                                                                                                                                                                                                                     microorganisms. Microbial species or genus or family or phylum or gwhich can be detected include Abiotrophia adiacems, Bordetella sp.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal bacterial, fungal and parasitical species in a test sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bergeron MG,
Picard FJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dentilication, algal, archaeal, bacterial, fungal, parasitical; microorganism, diagnosis, translation elongation factor Tu, toxin, translation elongation factor G, RecA recombinase, resistance; catalytic subunit of proton-translocating ATPase; antimicrobial, variating attention of the contraction 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 related microorganisms e.g. algae, archaea, bacteria, fungi and parasites, for universal detection and for specific and ubiquitous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 1035-1036; 1580pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-SEP-1999; 99CA-02283458.
19-MAY-2000; 2000CA-02307010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200123604-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention describes a method for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000WO-CA001150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boissinot M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           algal; archaeal; l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Huletsky A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; family specific; probe; bacterial; fungal; paras:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Menard C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antimicrobial; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouellette
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AAQ25183
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Best Local (
                                                                                             Matches
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25-MAR-2003
20-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptides involved in expression of glycopeptide antibiotic resistance - useful in diagnosing presence of Gram-positive enterococcal strains e.g. Enterococcus Faecium and E Gallinarum.
                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                  proteins encoded by the latter two genes (i.e. proteins VanR and have a regulatory function and control expression of the other th ("protective") proteins. See also AAQ25179-Q25182. (Updated on 25 2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PI (Updated on 25-MAR-2003 to correct PI (Updated on 26-MAR-2003 to correct PI (Updated on 27-MAR-2003 to correct PI (Updated on 28-MAR-2003 to correct P
                                                                                                                                                                                                                                                                                                                                                        This sequence contains the genes vanH, vanA, vanX, vanR and vanS.
                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 4; 163pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arthur M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-OCT-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INSP ) INST PASTEUR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D-Ala-D-Ala ligase; peptidoglycan precursor;
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                                                                                                                   Similarity
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                                                                                                                                                                                      7227 BP;
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                                             CCTATCCTGTTTTTGTTAAGCCGGCGC 27
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CCTATCCTGTTTTTGTTAAGCCGGCGC 5044
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                                                                                         100.0%;
ilarity 100.0%;
Conservative (
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                                                                                                                   Score 27;
Pred. No.
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Pred. No. 0.
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                                                                                                                                                                                      T; 0 U; 2 Other;
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                                                                                                                                         Length 7227;
                                                                                           Indels
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AAQ25178
ID AAQ2
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AAQ25178 standard;

DNA, 10851

AAQ25178;

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24-OCT-2003
25-MAR-2003
20-NOV-1992
                    Polypeptides involved in expression of glycopeptide antibiotic resistance - useful in diagnosing presence of Gram-positive enterococcal strains e.g. Enterococcus Faecium and B Gallinarum.
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                                                                                                                                                                                                                                                                                                                                                                                      Sab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycopeptide antibiotic; vancomycin; teicoplanin; resistant; D-Ala-D-Ala ligase; peptidoglycan precursor; transposon;
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       Claim 9;
                                                                      WPI; 1992-183677/22
                                                                                     Arthur M,
                                                                                                                    31-OCT-1990;
                                                                                                                                   29-OCT-1991;
                                                                                                                                                    14-MAY-1992.
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                                                            AAR24294, AAR24295, AAR24296,
      Fig
                                                     AAR24301,
                                                                                     Dukta-Malen S,
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(first en
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                                                                                                     PASTEUR.
                                                                                                                    90FR-00013579
                                                                                                                                    91WO-FR000855
      163pp; French
                                                                                                                                                                                                 complement (10814. .10851)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                    'product= "transposase"
                                                                                                                                                                                 'rpt_type= INVERTED
                                                                                                                                                                                                         product= "VanZ"
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*tag= 1
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                                                                                                                                                                                                                                                                                                                                                                       product= "VanR"
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                                                                                                                                                                                                                                 product= "VanY"
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                                                                                                                                                                                                                                                                                                                                                                                                      *tag=
                                                                                                                                                                                                                                                                                                       product= "VanH"
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                                                             AAR24297, AAR24298, AAR24299
                                                                                     Courvalin
                                                                                                                                                                                                                                                                                                                                                              activator"
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RASULT 21
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ID AAF76
XX AAF76
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XX BETT
XX II-AL
XX Redu
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The invention relates to methods of reducing vancomycin resistance in a CC vancomycin-resistant organism. One method involves introducing a CC vancomycin resistant organism. One method involves introducing a CC vancomycin resistance gene antisense nucleic acid into the organism; CC antisense oligonucleotides complementary to AAF76023-AAF76031 are CC particularly preferred for this purpose. The second method involves CC providing additional vanH promoter sequences which are not operatively CC coupled to a vancomycin resistance gene, so that the phosphorylated vanR CC gene product (which induces vanH promoter activity) is competitively CC sequestered. Both methods are able to restore antibiotic susceptibility CC in glycopeptide resistant enterococci. The methods of the invention are CC useful for reducing vancomycin resistance in a vancomycin resistant cC organism, particularly Enterococcus faecium and Enterococcus sp. and Streptococcus sp., to which Enterococcus faecium and Enterococcus sp. and CC faecalis have the potential to transfer resistance determinants. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             competitive inducer sequestration; vanH promoter; vanR gene product; Enterococcus; Staphylococcus; Streptococcus; Gram-positive bacterium; antibiotic susceptibility; ex vivo eradication; in vivo eradication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 24; Page 41-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reducing vancomycin-resistance in vancomycin-resistant introducing a antisense vancomycin-resistance molecule vancomycin-resistance gene expression, or by enhancing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterococcus faecium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glycopeptide resistance; VanA gene cluster;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vancomycin resistance reduction; antisense expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression.
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Pred. No.
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RESULT 22
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06-SEP-2001;
25-OCT-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               significant pathogens, and may be used for the ex vivo eradication of vancomycin-resistant enterococci from frequently colonised settings, such as intensive care units, heamodialysis units, and chronic care facilities, for the in vivo clearance of vancomycin- resistant enterococci from
the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of societies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                colonisation by vancomy significant pathogens,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antisense; ds; prokaryotic essential gene; cell proliferation; drug design; gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-FEB-2002;
                                                                                                                                                                                                                    Claim 14;
                                                                                                                                                                                                                                                           New antisense nucleic acids, useful for identifying for homologous nucleic acids required for cellular pisolate candidate molecules for rational drug disco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BLIT-)
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; 2001US-00948993.
; 2001US-0342923P.
; 2002US-00072851.
; 2002US-0362699P.
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Forsyth
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proliferation to
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Xu HH;
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AAX20248_07
Continuation
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AC 15-JU
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DB Enter
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Vancov
XW gene;
XW fluor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC the gene product or that has an activity against a biological pathway contentifying a gene required for cellular proliferation; (8) contentifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies cor a gene on which the test compound that inhibits proliferation of an corganism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene compound's activity; (11) a culture comprising strains in which the gene compound's activity; (11) a culture comprising strains in which the gene compound's activity; (11) a culture compound that inhibits the extent to which each of the strains is present in a culture or collection of continuous collection of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous mucleic acids required for cellular proliferation to isolate candidate molecules for rational cury discovery programs, or for screening homologous nucleic acids required continuous continuous. The present sequence is one of the target corporatyotic essential genes. Note: The sequence data for this patent did cont form part of the printed specification, but was obtained in celectronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                         RESULT 24
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Best Local S
Matches 22
                                                                                                                                                                                                                                                                                                                    Best
                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the polypeptide; (5) producing the polypeptide; proliferation or the activity of a gene in an o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1071 BP; 335 A; 127 C; 198 G; 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proliferation;
Vancomycin resistant enterococcus; vancomycin gene; ds; hospital acquired infection; VRE; fluorescence resonance energy transfer; FRET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
                                                                Enterococcus vancomycin resistance
                                                                                              15-JUL-2004
                                                                                                                                                             ADO47266 standard;
                                                                                                                                                                                                                                                                                                                                                                                  Fragment Name
AAX20248 00
AAX20248 02
AAX20248 02
AAX20248 03
AAX20248 03
AAX20248 05
AAX20248 06
AAX20248 06
AAX20248 06
AAX20248 06
AAX20248 06
AAX20248 08
                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                        10177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
                                                                                                                                                                                                                                        2 CTATCCTGTTTTTGTTAAGCCGGC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N
                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTATCCTGTTTTTGTTAAGCCGGC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTATCCTGTTATTGTTAAGCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of 10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 into
                                                                                                (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ne activity of a gene in an cidentifying a compound that
                                                                                                                                                             DNA; 555
                                                                                                entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.0%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX20248 from base 700001 fragments LOCUS AAX20248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Begin
                                                                                                                                                                                                                                                                                                                                      77.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                    600001
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                                                                                                                                                               ₽₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                       0;
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Pred. No. 21
                                                                                                                                                                                                                                                                                                                         Pred.
                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                                      710000
810000
910000
910715
                                                                                                                                                                                                                                                                                                                                                                                                                                  $10000
510000
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210000
310000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  End
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                           10200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              521
                                                                                                                                                                                                                                                                                                                         20.8;
No. 4
                                                                gene, vanB ENEVANB2A.
                                                                                                                                                                                                                                                                                                                                      DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ħ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0 U;
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                                                                                                                                                                                                                                                                                                       2
                                      resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Borrelia burgdorferi polynucleotide Accession Aax20248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (6) inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1071;
                                                                                                                                                                                                                                                                                                                                        Length 110000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               required
                                    gene; vanB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                          <u>.</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tor
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ADO47264/c
ID ADO472
XX
AC ADO472
XX
DT 15-JUL
XX Entero
XX Vancom
KW Vancom
KW Gene;
XW fluore
XX Entero
XX Entero
XX US2004
XX US2004
XX PD US2004
XX
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                                                                                                                                                                                                                                                                                                                                 RESULT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to detecting the presence or absence of vancomycin-
resistant enterococci (VRE) in a sample, comprising performing a cycling
step by amplifying a sample with pair of vanA or vanB primers and
hybridising the sample with a pair of vanA or vanB primers and
thou donor and acceptor fluorescent group, respectively, detecting
fluorescence resonance energy transfer (FRET), where the presence of FRET
indicates presence of VRE Also included is an article of manufacture,
comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
and a donor fluorescent group and a corresponding fluorescent group. The
method is useful for detecting the presence or absence of vanA or
resistant enterococci in a biological sample, e.g. stool samples, anal or
perirectal swabs, blood and body fluids from an individual. The method
creplaces standard culture methods and reduces the cost. The method
creplaces rapid vancomycin resistant enterococcus real time pCR assay
which is useful for beginning the antimicrobial therapy immediately to
treat hospital acquired infection. The presence can
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                     Vancomycin resistant enterococcus; vancomycin resistance gene; vanB; gene; ds; hospital acquired infection; VRE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detecting presence or absence of vancomycin-resistant enterococci in biological sample from individual comprises using real time polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cockerill FR, Sloan LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-SEP-2002; 2002US-00254260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2004058336-A1
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                                                                                                                                                                                      Enterococcus vancomycin resistance gene, vanB ENEVANB
                                                                                                                                                                                                                           15-JUL-2004
                                                                                                                                                                                                                                                             ADO47264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 555 BP; 132 A; 161 C; 115 G; 145 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 20; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-SEP-2002; 2002US-00254260
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                     25-MAR-2004.
                                                     US2004058336-A1
                                                                                   Enterococcus sp.
                                                                                                                       fluorescence
                                                                                                                                                                                                                                                                                           ADO47264 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     enterococcal vanB, vancomycin resistance gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (COCK/) COCKERILL F R. (SLOA/) SLOAN L M.
                                                                                                                                                                                                                                                                                                                                                                                   391
                                                                                                                                                                                                                                                                                                                                                                                                     1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                 CCTACCCTGTCTTTGTGAAGCCGGCAC 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                       resonance
                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.3%;
85.2%;
                                                                                                                     energy transfer;
                                                                                                                                                                                                                                                                                             556
                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 20.6;
Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
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RESULT 26
ADO477262/c
ID ADO47262 standard; DNA; 556 BF
XX
AC ADO47262;
XX

DE 15-JUL-2004 (first entry)
XX

DE 25-faecalis vancomycin resista
XX

Vancomycin resistant enterococc
XM
Vancomyci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                          Vancomycin resistant enterococcus; vancomycin resistance gene; vanB; gene; ds; hospital acquired infection; VRE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   E. faecalis vancomycin resistance gene, vanB EFU94526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 556 BP; 130 A; 154 C; 117 G; 155 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to detecting the presence or absence of vancomycin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 18; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting presence or absence of vancomycin-resistant enterococci in biological sample from individual comprises using real time polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-268785/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cockerill FR, Sloan LM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-SEP-2002; 2002US-00254260.
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                                                                                                                                                     25-SEP-2002; 2002US-00254260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   enterococcal vanB, vancomycin resistance gene.
                                                                                                       25-SEP-2002; 2002US-00254260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.3%;
                                                                                                                                                                                                                                                                                                                                                   energy transfer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 20.6;
Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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Cockerill

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Sloan

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cc resistant enterococci (VRE) in a sample, comprising performing a cycling c step by amplifying a sample with pair of vanA or vanB primers and cc hybridising the sample with a pair of vanA or vanB primers and cc hybridising the sample with a pair of vanA or vanB probes, labelled with c donor and acceptor fluorescent group, respectively, detecting c indicates presence of VRE. Also included is an article of manufacture, c comprising a pair of vanA or vanB probes c and a donor fluorescent group and a corresponding fluorescent group. The c method is useful for detecting the presence or absence of vanComycin-cc resistant enterococci in a biological sample, e.g. stool samples, anal or c method is useful for detecting the presence or absence of vanComycin-cc replaces standard culture methods and reduces the cost. The method creplaces standard culture methods and reduces the cost. The method crowides rapid vancomycin resistant enterococcus real time PCR assay c which is useful for beginning the antimicrobial therapy immediately to c treat hospital acquired infection. The present sequence is an content of the present sequence is an enterococcal vanB, vancomycin resistance gene.

The invention relates to detecting the presence or absence of vancomycin-resistant enterococci (VRE) in a sample, comprising performing a cycling

Disclosure; SEQ ID NO 15; 23pp; English.

Detecting presence or absence of vancomycin-resistant enterococci in biological sample from individual comprises using real time polymerase

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ARBSULT 27
ARD047263/c
ID 4D0472
XX AD0472
XX AD0472
XX Vancom
XW Vancom
XW Sentero
XX US2004
XX
                                       Detecting presence or absence of vancomycin-resistant enterococci biological sample from individual comprises using real time polym
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vancomycin resistant enterococcus; vancomycin gene; ds; hospital acquired infection; VRE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-SEP-2002; 2002US-00254260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-SEP-2002; 2002US-00254260.
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                                                                                                                                                                     2004-268785/25
                                                                                                                                                                                                                                                                                                                                  COCKERILL F R. SLOAN L M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     resonance energy transfer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                               Sloan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene;
                                       polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vanB;
                                                                          in
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392 CCTACCCTGTCTTTGTGAAGCCGGCAC 366 1 CCTATCCTGTTTTTGTTAAGCCGGCGC

Query Match Best Local & Matches

1 76.3%; Similarity 85.2%;

Score 20.6; DB Pred. No. 23; 0; Mismatches

DB 12; T; 0 U;

Length 556; 0 Other;

23;

Conservative

0;

4

Indels

<u>.</u>

Gaps

0

Sequence 556 BP; 133 A; 162

C; 116 G; 145

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                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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                                        B. faecalis vancomycin resistance gene, vanB EFU94529.
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 556 BP; 130 A; 154 C; 117 G; 155 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       method is useful for detecting the presence or absence of vancomycin-
resistant enterococci in a biological sample, e.g. stool samples, anal
perirectal swabs, blood and body fluids from an individual. The method
replaces standard culture methods and reduces the cost. The method
provides rapid vancomycin resistant enterococcus real time PCR assay
which is useful for beginning the antimicrobial therapy immediately to
treat hospital acquired infection. The present sequence is an
                                                                                 15-JUL-2004
                                                                                                                                                                   ADO47261 standard; DNA; 556
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                                                                                                                                                                                                                                                                      392
                                                                                                                                                                                                                                                                                                           1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                    CCTACCCTGTCTTTGTGAAGCCGGCAC 366
                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vanB, vancomycin resistance gene.
                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                   76.3%;
85.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to detecting
                                                                                                                                                                   BP.
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                                                                                                                                                                                                                                                                                                                                                                       Score 20.6; I
Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                    Mismatches
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    resistance
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gene;
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RESULT 28
AD047261/c
ID AD0472
XX AD0472
XX AD0472
XX Yancom
KW Gene;
KW Vancom
KW Gene;
KW Fluore
XX US2004
XX US20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fluorescence
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The invention relates to detecting the presence or absence of vancomycin-resistant enterococci (VRE) in a sample, comprising performing a cycling step by amplifying a sample with pair of vanA or vanB primers and hybridising the sample with a pair of vanA or vanB probes, labelled with

Detecting presence or absence of vancomycin-resistant enterococci in biological sample from individual comprises using real time polymeras

polymerase

Cockerill FR, Sloan

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Disclosure; SEQ ID NO

14; 23pp; English.

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RESULT 29
AD047265/c
ID AD0472;
XX
AC AD0472;
XX
AC AD0472;
XX
Concern Service Service
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Best Local S
Matches 23
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The invention relates to detecting the presence or absence of vancomycin-resistant enterococci (VRE) in a sample, comprising performing a cycling step by amplifying a sample with pair of vanA or vanB probes, labelled with donor and acceptor fluorescent group, respectively, detecting fluorescence resonance energy transfer (FRET), where the presence of FRET indicates presence of VRE. Also included is an article of manufacture, comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes and a donor fluorescent group and a corresponding fluorescent group. The method is useful for detecting the presence or absence of vancomycin-resistant enterococci in a biological sample, e.g. stool samples, anal or
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fluorescence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting presence or absence of vancomycin-resistant enterococci in biological sample from individual comprises using real time polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vancomycin resistant enterococcus; vancomycin resistance gene; vanB; gene; ds; hospital acquired infection; VRE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ID NO
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85.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   19; 23pp;
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
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RESULT 30
AD047260/c
ID AD0472
XX AD0472
XX AD0472
XX B. fae
XX Vancom
XW Gene;
XW Fluore
XX US2004
XX US2004
XX US2004
XX COCK;
PH (COCK)
PA (COCK)
PA (SLOA)
XX Detect
PT biolo;
YX Detect
YX Dete
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                            The invention relates to detecting the presence or absence of vancomycin-
CC resistant enterococci (VRE) in a sample, comprising performing a cycling
CC step by amplifying a sample with pair of vanA or vanB primers and
CC hybridising the sample with a pair of vanA or vanB primers and
CC donor and acceptor fluorescent group, respectively, detecting
CC fluorescence resonance energy transfer (FRET), where the presence of FRET
CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
CC and a donor fluorescent group and a corresponding fluorescent group. The
CC method is useful for detecting the presence or absence of vancomycin-
CC resistant enterococci in a biological sample, e.g. stool samples, anal or
CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanB, vancomycin resistance gene.
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Best Local S
Matches 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting presence or absence of vancomycin-resistant enterococci in biological sample from individual comprises using real time polymerase
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fluorescence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 13; 23pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chain reaction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            resonance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sloan LM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vancomycin resistance gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.3%;
85.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        energy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 20.6;
Pred. No. 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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S

Sequence 556 BP; 134 A; 161 C; 116 G; 145 T; 0 U; 0 Other;

Query Match Best Local Matches

Similarity

76.3**%**; 85.2**%**;

23;

Conservative

0

Pred. No. 23; 0; Mismatches Score 20.6;

4

0

Gaps

0

DB 12;

Length 556; Indels

밁 १

392

1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27

CCTACCCTGTCTTTGTGAAGCCGGCAC 366

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RESULT 31
ADO47259/c
ID ADO472
                                                                                           S
                            Query Match
Best Local S
Matches 23
                                                                                                                                                                                                                                       The invention relates to detecting the presence or absence of vancomycin-
resistant enterococci (VRB) in a sample, comprising performing a cycling
step by amplifying a sample with pair of vanA or vanB primers and
hybridising the sample with a pair of vanA or vanB probes, labelled with
donor and acceptor fluorescent group, respectively, detecting
fluorescence resonance energy transfer (FRET), where the presence of FRET
indicates presence of VRE. Also included is an article of manufacture,
comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
and a donor fluorescent group and a corresponding fluorescent group. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-SEP-2002; 2002US-00254260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2004058336-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterococcus faecalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fluorescence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vancomycin resistant enterococcus; vancomycin resistance gene; ds; hospital acquired infection; VRE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADO47259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADO47259 standard;
                                                                                                                                 method is useful for detecting the presence or absence of vancomycin-
resistant enterococci in a biological sample, e.g. stool samples, ana.
perirectal swabs, blood and body fluids from an individual. The method
replaces standard culture methods and reduces the cost. The method
provides rapid vancomycin resistant enterococcus real time PCR assay
which is useful for beginning the antimicrobial therapy immediately to
treat hospital acquired infection. The present sequence is an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cockerill FR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-268785/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (COCK/)
                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 16; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting presence or absence of vancomycin-resistant enterococci in biological sample from individual comprises using real time polymerase
                                                                                           Sequence
                                                                                                                         enterococcal vanB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     faecalis vancomycin resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COCKERILL F R. SLOAN L M.
                                                Similarity
    CCTATCCTGTTTTTGTTAAGCCGGCGC 27
                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002US-00254260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        resonance
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                                                                                             BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sloan LM;
                                                                                           134 A; 161 C; 116 G; 145 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA;
                                                                                                                           vancomycin resistance gene.
                                              76.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          energy transfer; FRET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВP
                                 0
                                 Score 20.6; I
Pred. No. 23;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene, vanB EFU94530.
                                                                 踞
                                                                12;
                                    4
                                                                                                0 Other;
                                                              Length 556;
                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene; vanB;
                                                                                                                                                          immediately to
                                    0
                                    Gaps
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R
                                      0
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Enterococcus 02-JUN-2005 ADY59941;

faecalis vanB DNA sequence

SEQ ID

NO:15

(first entry)

ADY59941 standard;

DNA; 630

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RESULT 32
AAQ69230
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                                                                                                                                                                                                                    RESULT 33
ADY59941
ID ADY59
XX
AC ADY59
XX
AC ADY59
DT 02-JU
XX
DB Enter
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                                                                                                                                                                         Best Loc
Matches
                                                                                                                                                                                             Query Match
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23-FBB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gram positive teicoplanin; a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterococcus faecalis vanB gene (internal, amplified fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ69230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ69230
                                                                                                                                                                                                                                                                                                                             New protein VanB involved in bacterial resistance to glyco-peptide(s) esp vancomycin, and related nucleic acid, vectors, transformed cells antibodies, for in vitro detection of resistant strains.
                                                                                                                                                                                                                                                                                                                                                                                                        Arthur M, Dutka-Malen
                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FR2699539-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                   The protein encoded by the vanB gene is implicated in resistance of Grapositive bacteria to glycopeptides, particularly to vancomycin. This resistance is inducible by Vancomycin but not by telcoplanin. Sequence AAQ69230 is a claimed internal fragment of the vanB gene. (Updated on 2
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1994-227159/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-DEC-1992;
                                                                                                                                                                                                                   Sequence 589 BP; 163 A; 124 C; 166 G; 136
                                                                                                                                                                                                                                         AAQ69230 is a claimed internal fragment MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                          Claim 8;
                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAR57150
                                                                                                                                                                                                                                                                                                                                                                                                                               (INSP ) INST PASTEUR.
                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   392
                                                                                                                                 165
                                                                                                                                                      μ.
                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                         Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTACCCIGICITIGIGAAGCCGGCAC 366
                                                                                                                                                     CCTATCCTGTTTTTGTTAAGCCGGCGC 27
                                                                                                                                 ccracccrercrrargaadccedcac 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s bacteria; inducible glycopeptide resistance; vancomycin;
antibiotic; vanB gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               faecalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
(first entry)
                                                                                                                                                                                                                                                                                                          28; 39pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   92FR-00015671.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92FR-00015671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/note= "amplified internal fragment of vanB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 589
                                                                                                                                                                                     85.2%;
                                                                                                                                                                                                 76.3%;
                                                                                                                                                                                                                                                                                                                                                                                                         S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               589
                                                                                                                                                                                                                                                                                                            French.
                                                                                                                                                                                                                                                                                                                                                                                                           Bvers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                          Score 20.6; I pred. No. 23; 0; Mismatches
                                                                                                                                                                             <u>.</u>
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                                                                                                                                                                                                                                                                                                                                                                                                           Courvalin
                                                                                                                                                                                                  DB
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                                                                                                                                                                                                  Length 589;
                                                                                                                                                                                                                       0 Other;
                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene"
                                                                                                                                                                               0
                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                        Gram-
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RESULT 34
ADY59942
ID ADY59
XX
AC ADY59
XY
AC ADY59
DT 02-JU
XX
Enter
XX
ENter
XX
Enter
XX
OS Enter
XX
US200
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                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oligonuclectide composition comprising a first oligonuclectide comprising sequences substantially corresponding to nucleotides 870-896, 851-868 or 898-917 of the vanA gene, or its complement or portion, or an cleotides 387-404, 406-423 or 426-446 of the vanB gene, or its complement or portion, where the oligonuclectide hybridizes under stringent hybridization conditions to vanA or vanB gene, or its comprising one or more oligonuclectide(s) specific for a vanA gene and/or vanB gene in a test sample, comprising the oligonuclectide mentioned above. The method and kit are useful for detecting and/or amplifying genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).

They may also be used in other industrial purposes, such as for quality control of food, water, pharmaceutical products or other products requiring microbiological control. The present sequence represents an enterococcus faecalis vanB nucleotide sequence from the present
                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method for detecting vancomycin resistance gene vanA and/or vanB nucleic acid molecules in a sample comprising contacting the sample with a vanA- and/or vanB-specific oligonucleotide probe or primer, and detecting or determining the presence or amount of hybrid formation or amplified nucleic acid. Also described: (1) an hybrid formation or amplified nucleic acid. Also described:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterococcus faecalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 630 BP; 163 A; 135 C; 187 G; 145 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; SEQ ID NO 15; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and/or vanB-specific oligonucleotide probes or primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-SEP-2003; 2003US-00661094.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-SEP-2003; 2003US-00661094.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2005058985-A1
                                                                         DNA detection; antibiotic-resistance; vancomycin; vanB; ds
                                                                                                               Enterococcus
                                                                                                                                                  02-JUN-2005
                                                                                                                                                                                       ADY59942
                                                                                                                                                                                                                         ADY59942 standard; DNA; 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DODG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA detection; antibiotic-resistance; vancomycin; vanB; ds
   US2005058985-A1
                                      Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                    185
                                                                                                                                                                                                                                                                                                                                                                                             23;
                                                                                                                                                                                                                                                                                                                                                         μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DODGSON K J
                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                         CCTATCCTGTTTTTGTTAAGCCGGCGC 27
                                                                                                                                                                                                                                                                                                                    CCTACCCTGTCTTTGTGAAGCCGGCAC 211
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                           faecalis vanB DNA sequence
                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                           76.3%;
85.2%;
                                                                                                                                                                                                                         ВP
                                                                                                                                                                                                                                                                                                                                                                                             <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                             Score 20.6;
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                             SEQ ID NO:16
                                                                                                                                                                                                                                                                                                                                                                                                                                DB 14;
                                                                                                                                                                                                                                                                                                                                                                                             4
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 630;
                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                             0
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RESULT 35
AAH01126
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8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method for detecting vancomycin resistance (C) gene vanA and/or vanB nucleic acid molecules in a sample comprising contacting the sample with a vanA- and/or vanB-specific oligonucleotide (C) probe or primer, and detecting or determining the presence or amount of hybrid formation or amplified nucleic acid. Also described: (1) an (2) oligonucleotide composition comprising a first oligonucleotide comprising sequences substantially corresponding to nucleotides 870-896, 851-868 or (2) sequences substantially corresponding to nucleotides 870-896, 851-868 or (2) oligonucleotide sagnature or portion, or an (2) oligonucleotide sagnature or portion, or an (2) oligonucleotide sagnature or portion, where the oligonucleotide hybridizes under (2) complement or portion, where the oligonucleotide hybridizes under (2) at the present hybridization conditions to vanA or vanB DNA; and (2) a kit (2) comprising one or more oligonucleotide(8) specific for a vanA gene and/or vanB gene in a test sample, comprising the oligonucleotide mentioned (2) above. The method and kit are useful for detecting and/or amplifying genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying antibiotic resistance genes (e.g. vancomycin-resistant enterococcus). (2) They may also be used in other industrial purposes, such as for quality control of food, water, pharmaceutical products or other products are the present an Errococcus faecalis vanB nucleotide sequence from the present an expersion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                               identification; algal; archaeal; bacterial; fungal; parasitical; microorganism; diagnosis; translation elongation factor Tu; toxin; translation elongation factor G; RecA recombinase; resistance; catalytic subunit of proton-translocating appared.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-and/or vanB-specific oligonucleotide probes or primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 783 BP; 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; SEQ ID NO 16; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2005-222218/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-SEP-2003; 2003US-00661094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-SEP-2003; 2003US-00661094.
                                                                                                                                                                                                          Enterococcus faecium nucleotide sequence SEQ ID NO:1117.
                                                                                                                                                                                                                                                 24-JUL-2001
                                                                                                                                                                                                                                                                                                                            AAH01126
                                 Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DODG/) DODGSON K J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                          392
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23;
                                                                         de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                          standard; DNA; 801
                                                                                                                                                                                                                                                                                                                                                                                                                        CCTACCCTGTCTTTGTGAAGCCGGCAC 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.3%;
85.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; 166 C; 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 20.6;
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G; 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        몂
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 783;
                                                                                               antimicrobial; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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WO200123604-A2

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RESULT 36
ADY59937/c
ID ADY599
XX
AC ADY599
XX
XX
D2-JUN
XX
D3 Entero
XX
DNA de
XX
DNA de
XX
Entero
XX
Entero
XX
Entero
XX
ENTERO
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                                                                                                                                                                                                                                                                                                                                                                 श्
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cc acids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be cused for producing probes and/or primers for detecting one or more crelated microorganisms e.g. algae, archaea, bacteria, fungi and garasitical species, for universal detection and for specific and ubiquitous cd detection and identification of an algal, archaeal, bacterial, fungal and comparasitical species, genus, family and group. A nucleic acid (I) obtained cc using the method of the invention can be used for the universal detection of any bacterium, fungus or parasitie in a sample and for the detection of at least one antimicrobial agent resistance gene or at least one toxin comparasity of the specific and ubiquitous detection and for identification of streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against cused to design a therapeutic agent which is effective against complete comparatisms. Microbial species or genus or family or phylum or group which can be detected include Abiotrophia adiacens, Bordetella sp., comprebacteriaceae family, Pseudomonads group, Escherichia coli, wycobacteriaceae family, Pseudomonads group, Escherichia coli, con hour and improved accuracy is also achieved. AAH00010 to AAH002304 represent nucleotide sequences and primers/probes which are given in the camplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a method for generating a repertory of nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal bacterial, fungal and parasitical species in a test sample.
  US2005058985-A1
                                      Enterococcus faecium
                                                                      DNA detection; antibiotic-resistance; vancomycin; vanB;
                                                                                                          Enterococcus faecium vanB DNA sequence SEQ ID NO:11
                                                                                                                                                    02-JUN-2005
                                                                                                                                                                                          ADY59937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                            ADY59937 standard; DNA; 801 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 1027; 1580pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-SEP-1999; 99CA-02283458.
19-MAY-2000; 2000CA-02307010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-245006/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Picard FJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-SEP-2000; 2000WO-CA001150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INFE-)
                                                                                                                                                                                                                                                                                                                             389
                                                                                                                                                                                                                                                                                                                                                                                                       23;
                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFECTIO DIAGNOSTIC (IDI)
                                                                                                                                                                                                                                                                                                                                                         CCTATCCTGTTTTTGTTAAGCCGGCGC 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               801 BP; 215 A; 169
                                                                                                                                                                                                                                                                                                                           CCTACCCTGTCTTTGTGAAGCCGGCAC 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Roy
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boissinot M, Huletsky A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PH;
                                                                                                                                                                                                                                                                                                                                                                                                                     76.3%;
85.2%;
                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                   Score 20.6; D
Pred. No. 25;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; 235 G; 182 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Menard C,
                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouellette M;
                                                                        gg
                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                  АДУ59940/с
                                                                                   RESULT 37
                                                                                                                                                                                                                                                                                                                                                 oligonucleotide composition comprising a first oligonucleotide comprising sequences substantially corresponding to nucleotides 870-896, 851-868 or 898-917 of the vanA gene, or its complement or portion, or an concleotide comprising sequences substantially corresponding to nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its complement profition, where the oligonucleotide hybridizes under comprising one or more oligonucleotide (s) specific for a vanA gene and/or stringent hybridization conditions to vanA or vanB DNA; and (2) a kit comprising one or more oligonucleotide(s) specific for a vanA gene and/or vanB gene in a test sample, comprising the oligonucleotide mentioned above. The method and kit are useful for detecting and/or amplifying genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying artibiotic resistance genes (e.g. vancomycin resistant enterococcus). They may also be used in other industrial purposes, such as for quality control of food, water, pharmaceutical products or other products or requiring microbiological control. The present sequence represents an Enterococcus faecium vanB nucleotide sequence from the present invention.
                                                                                                                                                                                                                                Query Match
Best Local S
Matches 23
                                                                                                                                                                                                                                                                                                                  Sequence 801
ADY59940;
                                         ADY59940 standard; DNA; 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene vanA and/or vanB nucleic acid molecules in a sample comprising contacting the sample with a vanA- and/or vanB-specific oligonucleotide probe or primer, and detecting or determining the presence or amount of hybrid formation or amplified nucleic acid. Also described: (1) an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method for detecting vancomycin resistance gene vanA and/or vanB nucleic acid molecules in a sample comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-and/or vanB-specific oligonucleotide probes or primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; SEQ ID NO 11; 33pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2005-222218/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-SEP-2003; 2003US-00661094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-SEP-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DODG/) DODGSON K J
                                                                                                                                                 413
                                                                                                                                                                                                                                23;
                                                                                                                                                                         بر .
                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                      CCTATCCTGTTTTTGTTAAGCCGGCGC 27
                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                BP; 181 A; 226 C; 169 G; 225 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2003US-00661094
                                                                                                                                                                                                                                                    76.3%;
                                         BP.
                                                                                                                                                                                                                                <u>.</u>
                                                                                                                                                                                                                                                    Score 20.6;
Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                      14;
                                                                                                                                                                                                                              4;
                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                        801;
                                                                                                                                                                                                                              0
                                                                                                                                                                                                                            Gaps
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#X#XBX#X8X#XBXAX#
                 12-SEP-2003; 2003US-00661094.
                                    17-MAR-2005
                                                                                                         Enterococcus faecium vanB DNA sequence SEQ ID NO:14.
                                                                                                                           02-JUN-2005
12-SEP-2003; 2003US-00661094
                                                                     Enterococcus faecium
                                                                                       DNA detection; antibiotic-resistance; vancomycin; vanB;
                                                                                                                           (first entry)
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gb

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ADY59943/c
ID ADY599
XX
ADY599
XC ADY599
XX
CONSEN
XX
CONSEN
XX
DNA de
XX
OS Enterc
OS Enterc
OS Enterc
SYNTHE
XX
US200:
XX
PI 17-MAI
XX
PF 12-SEI
XX
PR 12-SEI
XX
PR 100DG,
XX
PI Dodgs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              898-917 of the vanA gene, or its complement or portion, or an oligonuclectide comprising sequences substantially corresponding to nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its complement or portion, where the oligonuclectide hybridizes under stringent hybridization conditions to vanA or vanB DNA; and (2) a kit comprising one or more oligonuclectide(s) specific for a vanA gene and/or vanB gene in a test sample, comprising the oligonuclectide mentioned above. The method and kit are useful for detecting and/or amplifying genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying antibiotic resistance genes (e.g. vancomycin-resistant enterococcus). They may also be used in other industrial purposes, such as for quality control of food, water, pharmaceutical products or other products an orequiring microbiological control. The present sequence represents an enterococcus and products or other products and products or other products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a method for detecting vancomycin resistance gene vanA and/or vanB nucleic acid molecules in a sample comprising contacting the sample with a vanA- and/or vanB-specific oligonucleotide probe or primer, and detecting or determining the presence or amount of hybrid formation or amplified nucleic acid. Also described: (1) an oligonucleotide composition comprising a first oligonucleotide composition sequences substantially corresponding to nucleotides 870-896, 851-868 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-and/or vanB-specific oligonucleotide probes or primers.
                                                                                                                                                                                                                               Enterococcus faecalis. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 801 BP; 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; SEQ ID NO 14; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2005-222218/23.
                                                                                                                                                                                                                                                                       Enterococcus
                                                                                                                                                                                                                                                                                                           DNA detection; antibiotic-resistance; vancomycin; vanB;
                                                                                                                                                                                                                                                                                                                                                Consensus vanB DNA sequence SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                        02-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                           ADY59943;
 Dodgson KJ
                                                                             12-SEP-2003; 2003US-00661094
                                                                                                                12-SEP-2003; 2003US-00661094
                                                                                                                                                        17-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADY59943 standard; DNA; 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterococcus faecium vanB nucleotide sequence from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DODG/) DODGSON K J.
                                       (DODG/) DODGSON K J
                                                                                                                                                                                            US2005058985-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTATCCTGTTTTTGTTAAGCCGGCGC 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCTACCCTGTCTTTGTGAAGCCGGCAC 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                       faecium
                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; 234 C; 169 G; 215 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 20.6;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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WPI; 2005-222218/23.
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and/or vanB-specific oligonucleotide probes Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for identifying vancomycin-resistant enterococcus, comprises using vanAor primers.

Example 1; SEQ ID NO 17; 33pp; English.

probe or primer, and detecting or determining the presence or amount of hybrid formation or amplified nucleic acid. Also described: (1) an oligonucleotide composition comprising a first oligonucleotide composition comprising a first oligonucleotide comprising sequences substantially corresponding to nucleotides 870-896, 851-868 or oligonucleotide comprising sequences substantially corresponding to oligonucleotide comprising sequences substantially corresponding to nucleotides 387-404, 406-423 or 426-446 of the vans gene, or its complement or portion, where the oligonucleotide hybridizes under the ringent hybridization conditions to vans DNA; and (2) a kit comprising one or more oligonucleotide(8) specific for a vans gene and/or vans gene in a test sample, comprising the oligonucleotide mentioned above. The method and kit are useful for detecting and/or amplifying antibiotic resistance genes (e.g. vancomycin-resistant enterococcus). They may also be used in other industrial purposes, such as for quality control of food, water, pharmaceutical products or other products requiring microbiological control. The present sequence represents a consensus vans nucleotide sequence from the present invention. The invention relates to a method for detecting vancomycin resistance gene vanA and/or vanB nucleic acid molecules in a sample comprising contacting the sample with a vanA- and/or vanB-specific oligonuclectide contacting the sample with a vanA- and/or vanB-specific oligonuclectide contacting the presence or amount of

Sequence 801 BP; 181 A; 235 C; 169 G; 216 T; 0 U; 0 Other;

밁 á Matches Query Match Best Local (413 23; 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27 Similarity CCTACCCTGTCTTTGTGAAGCCGGCAC 387 Conservative 76.3%; 0, Score 20.6; Pred. No. 25; Mismatches B 14; 4. Length 801; 0 Gaps

0,

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RESULT 39
ADY59939/c
ID ADY599
XX ADY599
XX DATERO
ACT O2-JUN
XX DNA de
XX DNA de
XX DNA de
XX US2005
XX DDETECT
PT e.g.
PT e.g.
                                                                                                                                                                                                                                                                                                                  Enterococcus faecium vanB DNA sequence SEQ ID NO:13
                                                                                                                                                                                                                                                                                                                                               02-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                          ADY59939;
                                                                                                                                                                                                                                                                                                                                                                                                      ADY59939 standard; DNA; 801
                                                                                                                                                                                                                               US2005058985-A1
                                                                                                                                                                                                                                                           Enterococcus faecium
                                                                                                                                                                                                                                                                                       DNA detection; antibiotic-resistance; vancomycin; vanB; ds
                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                      ВP
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Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-and/or vanB-specific oligonucleotide probes or primers.

WPI; 2005-222218/23.

12-SEP-2003; 2003US-00661094.

12-SEP-2003; 2003US-00661094

(DODG/) DODGSON K J.

문 S XXXSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSXXXX Query Match Best Local ? Matches comprising one or more oligonucleotide(s) specific for a vanh gene and/or vanB gene in a test sample, comprising the oligonucleotide mentioned above. The method and kit are useful for detecting and/or amplifying genes (i.e. vanh and/or vanB genes) in a test sample, or for identifying antibiotic resistance genes (e.g. vancomycin-resistant enterococcus). They may also be used in other industrial purposes, such as for quality control of food, water, pharmaceutical products or other products control of food, water, pharmaceutical products or other products an equiring microbiological control. The present sequence represents an Enterococcus faecium vanB nucleotide sequence from the present invention. 17-MAR-2005 Enterococcus 02-JUN-2005 ADY59936 standard; DNA; 801 BP 12-SEP-2003; 2003US-00661094. US2005058985-A1. Enterococcus faecium Sequence 801 BP; 183 A; 234 C; 169 G; 215 T; 0 U; 0 Other; sequences substantially corresponding to nucleotides 870-896, 851-868 898-917 of the vanh gene, or its complement or portion, or an oligonucleotide comprising sequences provided to represent to nucleotide 387-404, 406-423 or 426-446 of the vanh gene, or its complement or portion, where the oligonucleotide hybridizes under stringent hybridization conditions to vanh or vanh DNA; and (2) a kit The invention relates to a method for detecting vancomycin resistance gene vanA and/or vanB nucleic acid molecules in a sample comprising contacting the sample with a vanA- and/or vanB-specific oligonucleotide probe or primer, and detecting or determining the presence or amount of ADY59936 oligonucleotide composition comprising a first oligonucleotide comprising sequences substantially corresponding to nucleotides 870-896, 851-868 or Example 1; brid formation or amplified nucleic acid. Also described: 413 23; μ Similarity CCTACCCTGTCTTTGTGAAGCCGGCAC 387 CCTATCCTGTTTTTGTTAAGCCGGCGC 27 SEQ ID NO 13; 33pp; English. Conservative (first entry) 85.2%; 76.3%; 0 Score 20.6; I Pred. No. 25; 0; Mismatches

멂 14; 4.

Length 801; Indels

0

Gaps

0

밁

413

CCTACCCTGTCTTTGTGAAGCCGGCAC 387

RESULT 40 ADY59936/c DNA detection; antibiotic-resistance; vancomycin; vanB; ds faecium vanB DNA sequence SEQ ID NO:10.

(DODG/) DODGSON K J

12-SEP-2003; 2003US-00661094

Dodgson

WPI; 2005-222218/23.

Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-and/or vanB-specific oligonucleotide probes or primers.

Example 1; SEQ ID NO 10; 33pp; English.

The invention relates to a method for detecting vancomycin resistance gene vanA and/or vanB nucleic acid molecules in a sample comprising contacting the sample with a vanA- and/or vanB-specific oligonucleotide

complement or portion, where the oligonucleotide hybridizes under stringent hybridization conditions to vanh or vanh DNA; and (2) a kit comprising one or more oligonucleotide(s) specific for a vanh gene and/or vanh gene in a test sample, comprising the oligonucleotide mentioned above. The method and kit are useful for detecting and/or amplifying genes (i.e. vanh and/or vanh genes) in a test sample, or for identifying antibiotic resistance genes (e.g. vancomycin-resistant enterococcus). They may also be used in other industrial purposes, such as for quality control of food, water, pharmaceutical products or other products control of food, water, pharmaceutical products or other products an Enterococcus faecium vanh nucleotide sequence from the present invention. probe or primer, and detecting or determining the presence or amount of hybrid formation or amplified nucleic acid. Also described: (1) an oligonucleotide composition comprising a first oligonucleotide comprisis sequences substantially corresponding to nucleotides 870-896, 851-868 or 898-917 of the vanA gene, or its complement or portion, or an 898-917 of the vanA gene, or its complement or portion, or an oligonucleotide comprising sequences substantially corresponding to nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its e comprising 851-868 or

(1) an

Sequence 801 BP; 182 A; 235 C; 169 G; 215 T; 0 U; 0 Other;

ફ Matches Query Match Best Local 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27 23; Similarity Conservative 76.3%; 85.2%; <u>.</u> Score 20.6; Pred. No. 2 Mismatches DB 14; 4. Length 801; Indels <u>,</u> Gaps

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Search completed: April Job time: 387.134 secs 9, 2006, 06:41:33

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Method and kit for identifying vancomycin-resistant enterococcus
Patent: WO 2005028679-A 3 31-WAR-2005;
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AY655719 Clostridi
AJ306726 Enterococc
AY958220 Enterococc
AY958270 Sequence
AN316727 Enterococc
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CS061877 Sequence
AN3167287 Sequence
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Z83305 E.faecium v
AP550667 Enterococc
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1 (bases 1 to 1029)

Arthur, M., Dukta-Malen, S., Molinas, C. and C Probes for the detection of nucleotide sequexpression of resistance to glycopeptides, gram-positive bacteria

Patent: US 5871910-A 3 16-FEB-1999;

Location/Qualifiers
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Khudaier, B.Y., Shafiani, S., Tewari, R. and Taneja, N.

Khudaier, B.Y., Shafiani, S., Tewari, R. and Taneja, N.

Detection and molecular characterization of vancomycin resistance

Detection and molecular characterization of vancomycin resistance
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                                 Similarity 27; Conserv
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                                                                                                                                                                                             Unknown.
Unclassified.
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mol_type="genomic DNA"
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le sequences implicated
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C12N5/10,
PC C12Q1/04,C12Q1/68,G01N33/53,G01N33/566,G01N33/569//C12P21/08,
PC (C12Q1/04,C12R1:01),(C12Q1/68,C12R1:01),C12N15/00,C12N5/00 CC
PC (C12Q1/04,C12R1:01), C12Q1/68,C12R1:01),C12N15/00,C12N5/00 CC
Polypeptides implicated in the expression of resistance to CC
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Paenibacillus thiaminolyticus D-alanyl-D-alanine ligase gene,
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Guardabassi,L., Christensen,H., Hasman,H. and Dalsgaard,A.
Members of the Genera Paenibacillus and Rhodococcus Harbor Genes
Homologous to Enterococcal Glycopeptide Resistance Genes vanA and
                                                                                                                                                   AY648035.1 GI:50082936
                                                                    Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus
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21-FEB-2002 JP 2002045484
31-OCT-1990 FR 90/135
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="unidentified"
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                                                                                                                                                                                 Submitted (09-UN-2004) Veterinary Pathobiology, The Veterinary and Agricultural University, Stigboejlen Frederiksberg C 1870, Denmark Location/Qualifiers
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Guardabassi, L., Hasm
Direct Submission
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KKIYKALGCRGLSRVDMFLQDNGSIVLNEVNTLPGFTSYSRYPRMVVAAGITLPELID
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Pred. No.
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db_xref="GI:50082943"

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AX111560
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Patent: WO 0112803-A 21 22-FEB-2001;
Beth Israel Deaconess Medical Center,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inouye,R.T., Torres-Viera,C., Moellering,R., Gold,H.
Bliopoulos,G.M.
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                                                                                                                                                  Enterococcus faecium
Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales;
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                                                        Highly conserved genes and their use to for detection of microorganisms
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                             Patent: WO 0123604-A 2293 05-APR-2001; Infectio Diagnostic (I.D.I.) INC. (CA)
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                                                                                          Picard, F.J. and Roy, P.H.
                                                                                                        Bergeron, M.G., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M.,
                                                                                                                                         Bitterococcus.
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Rsgvmggcekpcgdmdnencrsavlspekgheilituvedokgjolgridafsvlhegks
gedgalggipelsgipyvggddigsavcmdkslayiiakdgiaitpepwvigidepra
Aaaftypvfykparsgssygvkkyndadeldajiesargddskiliegapvlggergra
Vlgnsselivgevdqiruqhgifrihqeaepekgsenavitipadlsaeergrirdta
KKIYKALGCRGLarvdmflqdngrivlnevntlpgftsysryprmmvaagitlpelid
Location/Qualifiers
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/db_xref="taxon:1352"
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CQ797595
CQ797595.1
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AX110322
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Detection of vancomycin-resistant Enterococcus
Patent: Ep 1408120-A 9 14-APR-2004;
MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enterococcus faecium Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
                                                   Bergeron,M.G., Boissinot,M., Huletsky,A.
Picard,F.J. and Roy,P.H.
Picard, F.J. and Roy,P.H.
Highly conserved genes and their use to
for detection of microorganisms
Patent: WO 0123604-A 1055 05-APR-2001;
Infectio Diagnostic (I.D.; INC. (CA)
Location/Qualifiers
                                                                                                                                                                         Enterococcus gallinarum
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
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/mol_type="unassigned DNA"
/strain="BM4147"
/db_xref="taxon:1352"
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/organism="Enterococcus gallinarum"
/mol type="unassigned DNA"
/strain="R684"
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/db_xref="taxon:1352"
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                                                                                                                                       Bergeron,M.G., Boissinot,M., Huletsky,A., Picard,F.J. and Roy,P.H.
Highly conserved genes and their use to ge for detection of microorganisms Patent: WO 0123604-A 1052 05-APR-2001; Infectio Diagnostic (I.D.) INC. (CA) Location/Qualifiers
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Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
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Sequence 1052 from Patent WO0123604.
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Sequence 1054 from Patent WO0123604.
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Bacteria; Firmicutes; Lactobacillales;
                                                                                                                                                                                                                                                        Enterococcus.
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Similarity 100.0%;
27; Conservative (
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                                                                                   /organism="Enterococcus faecium"
/mol_type="unassigned DNA"
/strain="R492"
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                                                                     db_xref="taxon:1352"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Enterococcus faecalis"
mol_type="unassigned DNA"
db_xref="taxon:1351"
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AX110317
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Highly conserved genes and their use to ge for detection of microorganisms Patent: WO 0123604-A 1050 05-APR-2001; Infectio Diagnostic (I.D.) INC. (CA) Location/Qualifiers
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Sequence 1049 from Patent WO0123604.
AXII0316
AXII0316.1 GI:13926608
                                           . Similarity 100 27; Conservative
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Bacteria, Firmicutes, Lactobacillales, Enterococcaceae,
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Highly conserved genes and their use to
for detection of microorganisms
Patent: WO 0123604-A 1049 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
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Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
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                                                                                                         /organism="Enterococcus gallinarum"
/mol_type="unassigned DNA"
/strain="R691"
/db_xref="taxon:1353"
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/strain="R690"
/db_xref="taxon:1352"
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100.0%; Pred. No. 0.5;
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CCTATCCTGTTTTTGTTAAGCCGGCGC 616

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AX110320
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AX110323
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Highly conserved genes and their use to gene for detection of microorganisms patent: WO 0123604-A 1053 05-APR-2001; Infectio Diagnostic (I.D.I.) INC. (CA)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                         Enterococcus faecium
Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
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Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
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AX110320
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Highly conserved genes and their use to generate probes and primer for detection of microorganisms
Patent: WO 0123604-A 1056 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
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CCTATCCTGTTTTTGTTAAGCCGGCGC 618
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                                                      Conservative
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/mol_type="unassigned DNA"
/strain="R581"
/db_xref="taxon:1352"
                                                                                                                         /organism="Enterococcus faecium"
/mol_type="unassigned DNA"
/strain="R688"
/db_xref="taxon:1352"
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RESULT 17
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Sequence 1057 from Patent
AX110324
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Enterococcus flavescens
Bacteria; Firmicutes; Lactobacillales;
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Highly conserved genes and their use to
for detection of microorganisms
Patent: WO 0123604-A 1051 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
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Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
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/mol_type="unassigned DNA"
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                                                                                                                                                                             /organism="Enterococcus faecium"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (25-FRB-1991) S. Dutka-Malen, Institut Pasteur, Agents Antibacterions, 28 rue du Dr Roux, Paris Cedex 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dutka-Malen,S., Molinas,C., Arthur,M. and Courvalin,P. The VANA glycopeptide resistance protein is related to D-alanyl-D-alanine ligase cell wall biosynthesis enzymes Mol. Gen. Genet. 224 (3), 364-372 (1990)
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Bacteria; Pirmicutes; Lactobacillales;
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   Detection of vancomycin-resistant Enterococcus spp Patent: EP 1408120-A 10 14-APR-2004;
                               Cockerill, F.R. and Sloan, L.M.
                                                                                                              Enterococcus faecium
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KKIYKALGCRGLARVDMFLQDNGRIVLNEVNTLPGFTSYSRYPRMMAAAGIALPELID
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/product="VANA ligase"
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evidence=experimental
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Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales;
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CQ797597
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CS061873 1. GI:62553767
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                                                                                                     Method and kit for identifying vancomycin-resistant enterococcus
Patent: WO 2005028679-A 1 31-MAR-2005;
University of Iowa Research Foundation (US); DODGSON, Kirsty Jan
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Bacteria; Firmicutes; Lactobacillales;
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AR089411
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 Local Similarity hes 27; Conserv
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                                                                                                 1 (bases 1 to 2607)

1 (bases 1 to 2607)

Bergeron,M.G., Picard,F.J., Ouellette,M. and Roy,P.H.

Bergeron,M.G., Picard,F.J., Ouellette,M. and Roy,P.H.

Species-specific and universal DNA probes and amplification primers

to rapidly detect and identify common bacterial pathogens and

associated antibiotic resistance genes from clinical specimens for

routine diagnosis in microbiology laboratories

routine diagnosis in microbiology laboratories

Patent: US 5994066-A 170 30-NOV-1999;

Location/Qualifiers

1. 2607
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Highly conserved genes and their use to for detection of microorganisms Patent: WO 0123604-A 1139 05-APR-2001; Infectio Diagnostic (I.D.I.) INC. (CA) Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1768 bp | Sequence 1139 from Patent WO0123604.
                                                                                                                                                                                                                                                                                                                                  Sequence 170 from AR089411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales;
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100.0%; Score 27; DB 6; Length 2607; llarity 100.0%; Pred. No. 0.45; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Enterococcus faecium"
/mol_type="unassigned DNA"
/strain="BM4147"
/db_xref="taxon:1352"
                                                                                           organism="unknown"
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                                                                            mol_type="unassigned DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 27; DB 6
Pred. No. 0.48;
Mismatches
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5994066.
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AR093611
LOCUS
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AR035514
LOCUS
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 1518
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Sequence
AR035514
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Bergeron, M.G., Ouellette, M. and Roy, P.H.

Species specific and universal DNA probes and amplification primers to rapidly detect and identify common bacterial pathogens and associated antibiotic resistance genes from clinical specimens for routine diagnosis in microbiology laboratories

Patent: US 6001564-A 170 14-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
AR093611
                                                 27;
                                                                                                                                                             1 (bases 1 to 2667)
Arthur, M., Dukta-Malen, S., Molinas, C. and C Probes for the detection of nucleotide sequexpression of resistance to glycopeptides, gram-positive bacteria Patent: US 5871910-A 17 16-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                    1 CCTATCCTGTTTTTTTTTAAGCCGGCGC 27
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            CCTATCCTGTTTTTGTTAAGCCGGCGC 27
CCTATCCTGTTTTGTTAAGCCGGCGC 1544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="unknown"
/mol_type="unassigned DNA"
                                                                                                         /organism="unknown"
/mol_type="unassigned
                                                                                                                                     Location/Qualifiers
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from patent US 5871910.
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Pred. No. 0.45;
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                                                                                                                                                                                                  sequences implicated
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RESULT 27 BD181855

LOCUS DEFINITION

BD181855 2667 bp DNA linear PAT Polypeptides implicated in the expression of resistance glycopeptides, in particular in gram-positive bacteria,

PAT 15-MAY-2003

nucleotide

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SOURCE
ORGANISM
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AX110408
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Best Local S
Matches 27
                                                                                                                                             TITLE
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OS Bacteria
PN JP 2002320494
PD 05-NOV-2002
PP 21-FEB-2002 (
PR 31-OCT-1990 I
                                                                                   Highly conserved genes and their use to for detection of microorganisms Patent: WO 0123604-A 1141 05-APR-2001; Infectio Diagnostic (I.D.I.) INC. (CA)
                                                                                                                                                                                                                                                                                                                   3946 bp D
Sequence 1141 from Patent WO0123604.
AXII0408
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Enterococcus faecium
                                                                                                                                                                         Bergeron, M.G., Boissinot, M., Huletsky, A.,
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Arthur,M., DuktaMmalen,S., Molinas,C. and Courvalin,P.
Polypeptides implicated in the expression of resistance to
glycopeptides; in particular in gram-positive bacteria, nucleotide
sequence cod ing for these polypeptides and use for diagnosis
Patent: JP 2002320494-A 11 05-NOV-2002;
                                                                                                                                                         Picard, F.J. and Roy, P.H.
                                                                                                                                                                                                                           Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
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Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-FEB-2002 JP 2002045484
31-OCT-1990 FR 90/135
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05-NOV-2002
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/mol_type="unassigned
/strain="BM4147"
                                   organism="Enterococcus faecium"
                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism='Bacteria'.
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/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="unidentified"
|mol_type="genomic DNA"
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1. .2667
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Pred. No. 0.45;
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                                                                                                                                       generate probes and primers
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4654 bp DNA linear BCT 06-MAR-2005
Paenibacillus thiaminolyticus RSA1221 vanA resistance gene cluster,
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Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
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2048. .3016
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VMYLAHDIKTPLYSIIGYLSLLDEABMPVDQKAKYVHITLDKAYKLEQLIDEFFEIT
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                                                                                                                                                                                                                          db_xref="GI:60391956"
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                         gene="vans"
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RSA1221 vanA
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AR035512
                                                                                                                               1 (bases 1 to 7225)
Arthur,M., Dukta-Malen,S., Molinas,C. and Courvalin,P.
Probes for the detection of nucleotide sequences implicated expression of resistance to glycopeptides, in particular in gram-positive bacteria
Patent: US 5871910-A 15 16-FEB-1999;
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                                                                                                                                                                                                                                                        Unknown.
Unclassified.
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EMVSKGYVASKSSHSRGSAIDLTLYRLDTGELVPMGSGFDFMDERSHHAAKGISGNEA
QNRRCLRSIMENSGFEAYSFEWWHYVLRNEFYPNSYFDFFVK"
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kkiykalggrglsrvdmflqdngrivlnevntlpgftsysryprmmaaagitlpelid
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RMKQGAFIINTGRGFLVYTNELVKALENGKLGGAALDVLEGEEEFFYSDCSQKFIDNQ
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4046. .4654
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3009. .4040
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Paenibacillus apiarius
Paenibacillus apiarius
Bacteria; Firmicutes; Bacillales; Paenibacillaceae;
                                                               operon, complete sequen
DQ018711
DQ018711.1 GI:66731642
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Paenibacillus apiarius strain PA-B2B glycopeptide resistance vanA
Operon, complete sequence; and BtrU-like protein gene, partial cds.
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BD181853.1 GI:30792771
JP 2002320494-A/9.
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Arthur, M., DuktaMmalen, S., Molinas, C. and Courvalin, P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-FEB-2002 JP 2002045484
31-OCT-1990 FR 90/135
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    cod ing for
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Location/Qualifiers
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Paenibacillus.

gene	CDS	gene	CDS	CDS	gene	
/ Jenue " vanw" / operon= "glycopeptide resistance vanA" / operon= "glycopeptide resistance vanA" / codon_start=1 / trans[table=11 / trans[table=11 / product= "VanW-like protein" / product= "VanW-like protein" / protein_id= "AAY52011.1" / protein_id= "AAY52011.1" / db_xref="GI:66731645" / translation= "MTOIFPPLLPVRVMQRKMCFYAGMRFDGRRYABTIDGKOLPYKL / translation= "MTOIFPPLLPVRVMQRKMCFYAGMRFDGRRYABTIDGKOLPYKL / FEAGCALYNGNTGFDMAYQENKYFNLKLAAKTLNGLLIRPGGTFSFWRLVRHADKHIF / YKOGLTVTNGKKLTTAPGGGLCQMSNLLFWMFLHTPLTVTERSGHEVKERPERNSDEIK GVDATISEGWIDLKARNGTDCTYQISVAFDDENIIGTVFVDKRPQVLYRVANGGIEYS RESGGIYESVKVERAEIDSDTGBITGQKPLYTNKCKICYPLPENVEIKEAKKV" 31684136	/gene="vanW" /operon="glycopeptide resistance vanA" 2047.2862	/gene="vans" /operon="glycopeptide resistance vanA" /operon="glycopeptide resistance vanA" /note="sensor histidine kinase" /codon start=1 /transI table=11 /product="vanS" /protein id="AAY52010.1" /product="vanS" /protein id="AAY52010.1" /protein id="AAY52010.1" /b_xref="GI:66731644" /translation="MAIKLKNKNKNKTDYSKLKRKLYQYIVVIVMAAAVFVLFLRIF /KGTLGEWIVRFLENSYHLERQDAMIIYQYTIRNNIEIFIYVAIAISILILCRVMLSK PAKYPDEINTGIDILONDEDKQIELSAEMEFWEQKLNTLKRTLERGEDAKLAEQRKN DVVMYLAHDIKTFLTSVIGYLSLLDEAPDMFVEQKAKYVHITLDKAYRLEQLIDEFFE ITRYNLGYITITKKHIDLYYMLVQMADEFYFQLAANGSIFKDLAAIFEKFYRLDD ARSDTGGAGLGLAIAKGIIVQHGGGIYAESNDNYTTFTVELFALPDLVDKRSS" 20472862	/gene="vanS" /operon="glycopeptide resistance vanA" 674. 1840	Operons 919COPERING TESISHANCE VAIR" 1.696 / gene="vanR" / gene="vanR" / operons 919Copeptide resistance vanR" / operons 919Copeptide resistance vanR" / operons 1000 1000 1000 / note="response regulator" / codon start=1 / trans] table=11 / product="vanR" / product="va	resistance	<pre>1 (bases 1 to 9519) Guardabassi,L., Perichon,B., Van Heijenoort,J., Blanot,D. and Courvalin,P. Glycopeptide resistance van operons in Paenibacillus from soil unpublished 2 (bases 1 to 9519) Guardabassi,L., Perichon,B., Van Heijenoort,J., Blanot,D. and Courvalin,P. Guardabassi,L., Perichon,B., Van Heijenoort,J., Blanot,D. and Courvalin,P. Direct Submission Submitted (26-APR-2005) Unite des Agents Antibacteriens, Institut Pasteur, 25 rue du Docteur Roux, Paris 75015, France Location/Qualifiers 1. 9519 /organism="Paenibacillus apiarius" /mol type="genomic DNA" /mol type="genomic DNA" /strain="PA-B2B" /isolation_source="soil" /db_xref="taxon:46240"</pre>
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TITLE
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27; Conserv
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Guardabassi, L., Peri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Paenibacillus thiaminolyticus
Paenibacillus thiaminolyticus
Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
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                                                                                                                                                                                                                                                                                                       Submitted
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ted (26-APR-2005) Unite des Agents Antibacteriens,
                                                                                                                                                                                                                                                                25 rue du Docteur Roux,
Location/Qualifiers
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esdtoltalsfyndpelaaidtpngrvoflomigitgdeleamotmytlgvlstgloy
mpyyitdlerasllaisavseavhtomgtegsntgflfvshlamepgkkgmlsktpst
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Lactococcus lactis"
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                                                                                                                                                                                        /mol_type="genomic DNA"
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'note="telcoplanin resistance protein"

'codon start=1

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                                                                                                                                                                                                                             organism="Paenibacillus thiaminolyticus"
                                                                                                                                               isolation_source="soil"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MPYALGGPDPLDGISAYKADRPNPHWHFVTYGFSELYDKESDNT
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EPSILRILCENKGNVVSSEQLFHEIMGDEYFSKSNNTITVHIRHLREKMNDTIDNPKY
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DESVLFNGYKLFAVDGTDLKLFTNDKDSESYKKNESNTKGYKLVHIDANYDLKHHYYK
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5109. .6077
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AVGLVNLHSKKPSSMLQEVFSR F I LYNFSAL I AHQAQ I PNEATKR I NFSAAML I CRQY
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SSDTGGAGLGLAIAKEIIVQHGGQIYABSNDNYTTFTVELFALFDLVDKRSS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /operon="glycopeptide resistance vanA"
3721. .4881
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note="response regulator"
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                                                                                             protein_id="AAY52004.1"
db_xref="GI:66731637"
                                                                                                                                                                                                                                                  operon="glycopeptide
note="dehydrogenase"
                                                                                                                                                                                                                                                                                                                                                                                                              gene="vanH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           product="Vans"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="vanS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="vanR"
                                                                                                                                                                                                                                                                                                                   gene="vanH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 109. .6077
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VIERLRGFGCHVLAYDRSQKIEANYVPFDALLQNSDIVTLHVPLNADTRHIIGHEQIK

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ORIGIN
  Query Match
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YMSKGIADKOFSKVVNDAVKEGKWILKNAKKYGFILHYVPKDKTDVTGIQYEBHNIRVGF
SGLSLDVGSSLIKMERAPEKKWILKNAKKYGFILHYVPKDKTDVTGIQYEBHNIRVGF
PHSAIMKEKNFALEEYMDFLKEQKSITTTIDHQVYKIFYYPISQNTTIHVPANGQYEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAY52005.1"
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/transl_table=11
                                                                                                                                                                                                                                                                                     /operon="glycopeptide resistance vanA"
9108. .>9537
'gene="vanZ"
                                                                                                                                                                                                                                                                                                                                                                                                SGNNMDGVIVTVYSGKRD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAY52007.1"
/db_xref="GI:66731640"
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/note="D,D-carboxypeptidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKIYKALGCRGLSRVDMFLQDNGSIVLNBVNTLPGFTSYSRYPRMVAAGITLPBLID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CFGVWKMCEKPCAEWENSNCYSAVLSPDKKMHGLLVKKNHEYEIHHVDVAFSVLHGKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/transl_table=
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FLKLQRMPNVI ITPHTAYYTEQALRDTVEKTIKNCLDFERSQEHE"
                                                                                                                                                                                                                                           operon="glycopeptide resistance vanA"
note="teicoplanin resistance protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product="Vany"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein_id="AAY52006.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product="VanX"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="vanX"
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note="D-Ala:D-Lac ligase"
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SKGYVASKSSHSRGSAIDLTLYRLDTGELVPMGSGFDFMDERSHHAAKGISGNEA
  100.0%;
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  Score
  27;
DB 1;
Length 9537;
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VERSION
KEYWORDS
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PUBMED
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AUTHORS
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AUTHORS
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PUBMED
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Best Local Similarity 100. Matches 27; Conservative
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J. Bacteriol. 175 (1), 117-127 (1993)
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10851 bp DNA Linear BCT 20-JUN-21
Enterococcus faecium transposon Th1546 transposase, resolvase, ver
(vanR), vanS (vanS), vanH (vanH), vanA (vanA), vanX (vanX), vanY
(vanY), and teicoplanin resistance protein (vanZ) genes, complete
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The vanZ gene of Tn1546 from
resistance to teicoplanin
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Arthur, M., Molinas, C.,
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                                                                                                                                                                                                                                                  NKRYSILTIYLLQLTQELTDKAFEIHDRQILSLLSKGRKAQEEIQKQNGKKLNEKVĪH
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SDGMEMQLGVSSLHADANPHYGTGKGATITRFTSDGFSSYYTKIIHTNSRAHHLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LWDHLKEIRSEYDFYTFTLSEYRMTFKYLHQLALENGDAIHLLHECIDFLRKNKIILP
AITTLERMYWEARAMAEKKLFNTVSKSLTNEQKEKLEGIITSQHPSESNKTILGWLKE
PPGHPSPETFLKIIERLEYIRGMDLETVQISHLHRNRLLQLSRLGSRYEFYAFRDFQE
                                                     mgr i ekt i fi lny i sdeslkrki qrglinkgeamnglara i ffgkqgelkert i qhqlq
rasalni i ina i s imntlhl ttaveykkrtgspnedllhhmsplgweh i nllgbyhfn
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RREENRLGFAVQLAVLRYPGMPYTHIKSIPDSVIQYISKGJGVST
RREENRATIONSVIQYISKGJGVST
RREENRATIONSVIQYISKGJGVST
RREENRATIONSVIQYISKGJGVST
RREENRATIONSVIQYISKGJGT
RREENRATI
SEKVVSLNSLRPLKLS"
                                                                                                                                                                 KLEAILRGQINTKVIKENYEDVLRLAHSIREGTVSASLINGKLGSYSRQNSLATALRE
                                                                                                                                                                                                                  SLLHHBTDLNI BEHYTDTAGYTDQI FGLTHLI
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/transposon="Tn1546"
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/mol_type="genomic DNA"
/specimen voucher="BM4147"
/db_xref="taxon:1352"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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|. .10851
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6979. .8010
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6018. .6986
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                                     id="AAA65957.1"
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Conservative

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AR035513
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AR035513
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27; Conserv
                                                                                                                            1 (bases 1 to 10851)
Arthur,M., Dukta-Malen,S., Molinas,C. and Courvalin,P.
Archer for the detection of nucleotide sequences implicated expression of resistance to glycopeptides, in particular in gram-positive bacteria
Patent: US 5871910-A 16 16-FEB-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                     Unknown
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 Similarity
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100.0%; Score 27;
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100.0%; Pred. No. 0.37;
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US 5871910
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                 DB_6; Length 10851;
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OS Bacteria
PN JP 2002320494
PN JP 200232002
PD 05-NOV-2002
PP 21-PBB-2002
PR 31-OCT-1990 IP
PI MICHEL ARTHUI
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C12N5/10,
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Sequence 1 from Patent W00112803.
XX085648
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Inouye, R.T., Torres-Viera Eliopoulos, G.M. Methods and compositions glycopeptide-resistant En
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polypeptides implicated in the expression of resistance to glycopeptides, in particular in gram-positive bacteria, nucleotide sequence cod ing for these polypeptides and use for diagnosis. BD181854
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Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales;
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Arthur, M., Duktammalen, S.,
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CC (C12Q1/04,C12R1:01),(C12Q1/68,C12R1:01),C12N15/00,C12N5/00 CC
Polypeptides implicated in the expression of resistance to CC glycopeptides,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              these polypeptides and use for diagnosis
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Location/Qualifiers
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Enterococcus faecium plasmid pUW786
gene cluster, complete sequence.
AF516335
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Enterococcus faecium
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Direct Submission
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Werner,G., Klare,I.
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  complement (6335. .7143)
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KILPRVLMVDEFRSHASIEDKMSFICADGETGKLIDVLPTRKLPRLTSYFFGGTNEE
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QAEKLKKNWRFILKNEANINHYEYKTWKSFFARKYPFLTEAMNIDRLLEFSPFLKEAY
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                                                        9594. .9613
/note="IR-R"
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complement(join(9287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9136. .>17510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVNNLSTVTYEQVLSIFNSYLLFNGRK"
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                                                                                                              insertion_seq="IS150-like"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(9287. .9592,11012. .12001))
note="coding region disrupted by insertion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="IS1182 IR-R"
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|ab_xref="GI:21886746"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product="unknown"
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transl_table=11
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JOURNAL REFERENCE
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AUTHORS
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AE017171
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TITLE
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gill, S., Kolonay, J., Shetty, J., Tenover, F. and Weigel, L. Sequence of the Michigan vancomycin-resistant Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Medical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ubmitted (30-JUL-2003) The Institute for Genomic Research, 9712
edical Center Dr., Rockville, MD 20850, USA
    Location(Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTATCCTGTTTTTTTTAAGCCGGCGC 4267
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YLNNLIEQDHRHIKVRKTRYQSINTĀKNTLKGIECIYALYKKNRRSLQIYGFSPCHEI
SIMLAS"
                                     STVYRWVQEYAPILYQIWKKKHKKAYYKWRIDETYIKIKGKWSYLYRAIDAEGHTLDI
STVYRWVQEYAPILKQIWKKKHKKAYYKWRIDETYIKIKGKWSYLYRAIDAEGHTLDI
                                                                                                                                                                                                                                                                                                          KKQBKVANMEGYLMRSIIABLBEMHSTIMRRKNMENNPLSLFN"
                                                                                                                                                                                                                                                                                                                                eliksyinnesybevksiksvilkakksennkydteymledideelllvlkrekgylv
                                                                                                                                                                                                                                                                                                                                                                   NKPNLLYLLKPAITKNDIYBIDKAENEVBALQDKEVSKGHVQKCQKDTSRNVKRTRLE
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protein_id="AAQ17125.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                           product="replication initiator protein"
protein_id="AAQ17124.1"
db_xref="GI:33390918"
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yy sequence similarity; putative"
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                                                                                                                                                                                                           note=\overline{n}similar to GP:13383313,
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transl_table=11
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                                                                           translation="MNYFRYKQFNKDVITVAVGYYLRYALSYRDISEILRGRGVNVHH
                                                                                                                                                    transI_table=11
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Pred. No. 0.34;
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/locus tag="VRA0007" /note="similar to GP:21623785; identified by sequence similarity; putative"
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SHMVDGNITVIDSKSISFGLGYQIXQIVELVLLQSKKI"
                                                                                                                                                                                                                                                             /translation="MNYFRYKQFNKDVITVAVGYYLRYALSYRDISEILRGRGVNVHH
STVYRWVQEYAPILYQIWKKKHKKAYYKWRIDETYIKIKGKWSYLYRAIDAEGHTLDI
WLRKQRDNHSAYAPIKRLIKQFGKPQKVITDQAPSTKVAWAKVIKAFKLKEDCHCTSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MYNPPDEAYHGLCESILEIGNRALDRTHTGTISKFGHQLARDLT
KGFPLLTTKKVSEKLVATELLAWIKGSTNIQYLLKYNNNIAHAFENYVGSDDYHGP
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GNHYDQLKSVIQQIKTNPNSRRHIVSAWNPTEIDSMALPPCHTMPQPYVQEGKLACQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /trānslation="MTLSIIVAHDKQRVIGYQNQLPWHLPNDLKHIKQLTTGNTLVMA
RKTFNSIGKPLPNRRNVVLTNQASFHHEGVDVINSLDBIKELSGHVFIFGGQTLYEAM
IDQVDDMYITVIDGKFQGDTFFPPYTFENWEVESSVEGQLDEKNTIPHTFLHLVRRKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to GP:13383309,
by sequence similarity; putati
                                                                                                                                                                                    complement (4697.
                                                                                                                                                                                                                 SIMLAS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence similarity;
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/codon atart-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (2317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (2317. .2802)
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/locus_tag="VRA0003"
/note="similar to GP:4105402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (1885.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /locus_tag="VRA0006"
/note="similar to SP:P14506,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rdsylppqlkintdksifdinyedlelinyeshpaikapiav"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transI_table=11
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/protein_id="AAQ17128.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="thyA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="trimethoprim resistant dihydrofolate reductase"
/protein_id="AAQ17127.1"
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protein_id="AAQ17126.1"
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                                                                                                                                                                                                                                                                                                                                                                                      product="IS431mec transposase"
                                                                                                                                                                                                                                                                                                                                                                                                              transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Locus_tag="VRA0006"
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                                                                                  gene="artA"
                                                                                                                                   locus_tag="VRA0007"
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                                                                                                                                                                                                                                                                                                                                     db_xref="GI:33390923"
                                                                                                                                                                                                                                                                                                                                                               protein_id="AAQ17129.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
                                                                                                                                                                                                                                      _NNLIEQDHRHIKVRKTRYQSINTAKNTLKGIECIYALYKKNRRSLQIYGFSPCHBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .ocus_tag="VRA0004"
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                                                27;
                                                                     Similarity
CCTATCCTGTTTTTGTTAAGCCGGCGC 27
                                         100.0%;
ilarity 100.0%;
Conservative 0
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by sequence similarity; putative"
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/note="similar to GP:3676437; identified by sequence
similarity; putative"
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EDLALSLGLTATALKGNINISNVEKVTDNESMVTIENEINGKSEHLISDFKDSFIEKA
KEKLTVSPSMRLGFEEFKNASGQIAMGFTEFFGARYDESTLENDPKVVATEKGYSVSV
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SP:P15951, SP:P35030, and PID:37460; identified by
sequence similarity; putative"
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/translation="MSVEQEVKOIMLLNTGEWVFIVGLIFGLTIYGLLTIRPISTKEN
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/locus_tag="VRA0010"
6425. ..6832
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tglivavgicagvwivlkklpgiddpmvknemfrgvgmvlagvavgaalvwivpwvyn
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/note="similar to GP:3676436; identified by sequence
similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAQ17131.1"
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IKGIATDKKENKLVMAEDREDKQKVLLYANKDNDMYYLNSGSTYKEAVQNTFGNETNY
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/transI_table=11
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/protein_id="AAQ17130.1"
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819. .7502
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148. .6365
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                                             <u>,</u>
                                                                 Score 27; DB 1
Pred. No. 0.29;
                                             Mismatches
                                                                                         DB 1; Length 57889;
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                                             Indels
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RESULT 40
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SOURCE
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VERSION
Search completed: April Job time : 1052.14 secs
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                                                                                                                                                                    Local
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vanA gene cluster in a vancomycin-resistant clinical isolate
Bacillus circulans
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Bacillus circulans
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                                                                            CCTATCCTGTTTTTGTTAAGCCTGCGC 542
                                                                                                               CCTATCCTGTTTTTGTTAAGCCGGCGC 27
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                                                                                                                                                    Conservative
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Pred. No. 2.6;
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8, 37100 Verona, ITALY
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Maximum DB
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Maximum Match
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    nucleic search, using sw model
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Match
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  ADY59929

AAH02300

AAP76039

AAH01064

AAH01063

AAH01058

AAH01059

AAH01062

AAH01066

AAH01066

AAH01066

AAH01066

AAH01066

AAH01148

ADO47257

ADY59927

ADY59927

ADY59927

AAH28569

AAH01150
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        Aah01066 Enterococ
Aah011060 Enterococ
Aah01148 Enterococ
Ad047257 E. faeciu
Ady59927 Enterococ
Aat285994 Antibioti
Aah01150 Enterococ
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Aah01059
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ADT42360
ABQ99654
ACA45223
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AAH01720
AAH01720
AAF76048
ADY59931
AAQ69235
AAF76020
AAX12998
ABS98793
AAAS98199
ACA52513
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ADY59941
ADY59941
ADY59943
AAH01126
ADY59937
ADY59943
ADY59943
ADY59939
ADY59936
ADY59936
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ADY59936
 ADQ06950
ABV46718
ACH96095
ADX11876
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ACL36388
AAH01601
AAF76056
AEB26980
AAF76022
AAS81838
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AAF76019
ACA22997
AAX20248
AD047266
AD047264
AD047262
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ADO47259
Aah01601 Enterococ
Aaf76056 Enterococ
Aaf76056 Enterococ
Aaf76052 B. faeciu
Aaf76022 B. faeciu
Aas81838 DNA encod
Aas52598 B. coli D
Adt48822 Bacterial
Adt482360 Bacterial
Adt49360 Bacterial
Add99654 Human mem
Aca45232 Prokaryot
Adq21125 Human dia
Adq25127 Human sof
Adc81391 Carbonyl
Adc81391 Carbonyl
Adc81397 Carbonyl
Adc81398 Human can
Add13358 Human not
Add06946 Soybean t
Add06946 Soybean t
Add06945 Soybean t
Abv46718 Human pro
Acd96950 Soybean t
Abv46718 Human pro
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Ady59937 Enterococ
Ady59940 Enterococ
Ady59943 Consensus
Ady59939 Enterococ
Ady59936 Enterococ
Ady59938 Enterococ
Ady59938 Enterococ
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Aaf76048 Enterococ
Ady59931 Enterococ
Adc90583 E. faeciu
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Ady59942 Enterococ
Aah01126 Enterococ
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Ado47264 Enterococ
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Ado47263 E. faecal
Ado47261 E. faecal
Ado47265 E. faecal
Ado47260 E. faecal
Ado47260 E. faecal
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Aaf76020
Aax12998
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Aah02303
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Aca22997
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Aca52513 Prokaryot
Aax20535 Polynucle
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Continuation (8 of
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ADO62241
ABD12733
             ACF65384_3
ABD33102
                                                                                                                AAD48290
AAS07380
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AAT42134
                                              ADA02507
                                                                  ADX60608
ADO63288
ADO62242
ADX53082
ABD12707
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                                                                                                             ABS73149
                        ADE95755
ADZ12503
ADS73531
ACF67367
                                                                                                         ACF68191
                                                           ABD12689
                                                              ADO62245
ALIGNMENTS
                                                                                       Aah34587 Human col
Aaz54529 Neisseria
Ado62241 Transcrip
Abd12733 Pseudomon
                                 Ada02507 Mouse Wint
Adb72245 Mouse Wint
Ade95755 Mouse Wint
Adz12503 Murine ca
                                                                  Abd12733 Pseudomon
Adx60608 Pranscrip
Ado63288 Transcrip
Ado63242 Transcrip
Adx53082 Plant ful
Abd12707 Pseudomon
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Aav17622 P
                Ads73531 tcp gene
Continuation (10 o
Continuation (4 of
Abd33102 Murine ca
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Acf68191 Photorhab
                                                  Aav17622 Pisum sat
Aav06585 Arabidops
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Ado62245 Transcrip
             Acn44148 Mouse
                                                                                                                Human
Human
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                                                         Pseudomon
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CEA
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RESULT 1
AD75929
ID AD75929
AC AD75
AC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dodgson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-SEP-2003; 2003US-00661094.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DODG/) DODGSON K J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         faecium vanA probe SEQ ID NO:3
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The invention relates to a method for detecting vancomycin resistance gene vanA and/or vanB nucleic acid molecules in a sample comprising contacting the sample with a vanA- and/or vanB-specific oligonucleotide probe or primer, and detecting or determining the presence or amount of hybrid formation or amplified nucleic acid. Also described: (1) an

The present invention describes a method for generating a repertory of nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic

Disclosure; Page 1578; 1580pp; English.

Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal, bacterial, fungal and parasitical species in a test sample.

Detecting vanA and/or vanB nucleic acid molecules in a sample, usefue.g. identifying vancomycin-resistant enterococcus, comprises using and/or vanB-specific oligonucleotide probes or primers.

useful for using vanA-

SEQ ID

NO 3; 33pp; English.

WPI; 2005-222218/23.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oligonucleotide composition comprising a first oligonucleotide comprising sequences substantially corresponding to nucleotides %70-896, 851-868 or 898-917 of the vanh gene, or its complement or portion, or an concleotide 387-404, 406-423 or 426-446 of the vanh gene, or its complement or portion, or an complement or portion, where the oligonucleotide hybridizes under comprising one or more oligonucleotide hybridizes under comprising one or more oligonucleotide(s) specific for a vanh gene and/or vanh gene in a test sample, comprising the oligonucleotide manifold concerns the method and kit are useful for detecting and/or applifying genes (i.e. vanh and/or vanh genes) in a test sample, or for identifying antiblotic resistance genes (e.g. vancomycin-resistant enterococcus). They may also be used in other industrial purposes, such as for quality control of food, water, pharmaceutical products or other products a probe for Enterococcus faecium vanh, which is used in an example from the
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Best Local (
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                                                                                                                                                                     Bergeron MG,
Picard FJ,
                                                                                                                                                                                                                                          28-SEP-1999; 99CA-02283458.
19-MAY-2000; 2000CA-02307010.
                                                                                                                                                                                                                                                                                     28-SEP-2000; 2000WO-CA001150.
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                                                                                                                                                                                                                                                                                                                                                                       Enterococcus faecium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH02300;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 27 BP; 3 A; 8 C; 6 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention.
                                                                                                                                         WPI; 2001-245006/25
                                                                                                                                                                                                                                                                                                                                             WO200123604-A2
                                                                                                                                                                                                                                                                                                                                                                                                                catalytic
                                                                                                                                                                                                                 (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27;
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                                                                                                                                                                     PH;
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                                                                                                                                                                                   Huletsky A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 27;
Pred. No.
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-AUG-2000; 2000WO-US022086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enterococcus faecium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibiotic susceptibility; ex vivo eradication; glycopeptide resistance; VanA gene cluster; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  competitive inducer sequestration; vanH promoter; vanR gene product; Enterococcus; Staphylococcus; Streptococcus; Gram-positive bacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vancomycin resistance reduction; antisense expression inhibition
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-MAY-2001
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                                                                                                                                                                                                                                                                                                                                Inouye RT,
                                                                                                                                                                                                                                                                                                                                                                                                    (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
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                                                                                                                                                                                                                                                                                                                                Torres-Viera C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 27;
100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                    Gold H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in vivo eradication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0 Other;
                                                                                                                                                                                                                                                                                                                                Eliopoulos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ç,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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sequestered. Both methods are able to restore antibiotic susceptibility in glycopeptide resistant enterococci. The methods of the invention are useful for reducing vancomycin resistance in a vancomycin resistant organism, particularly Enterococcus faecium and Enterococcus faecalis, but also in other Gram-positive bacteria such as Staphylococcus sp. and Streptococcus sp., to which Enterococcus faecium and Enterococcus faecalis have the potential to transfer resistance determinants. The antisense molecules are useful in the treatment of infection and
                                                                             as intensive care units, haemodialysis units, and chronic care facilities; for the in vivo clearance of vancomycin- resistant enterococci from colonised gastrointestinal or genitourinary tracts of animals, including humans; and in primary or adjuvant therapy for vancomycin-resistant enterococcal infections. The gene based strategy targets key vancomycin resistance determinants and results in restoration of vancomycin susceptibility in previously glycopeptide- resistant enterococci. Sequences AAF67036-AAF67042 represent genes of the Enterococcus faecium vana cene cluster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            particularly preferred for this purpose. The second method involves providing additional vanH promoter sequences which are not operatively coupled to a vancomycin resistance gene, so that the phosphorylated vank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to methods of reducing vancomycin resistance in vancomycin-resistant organism. One method involves introducing a vancomycin-resistance gene antisense nucleic acid into the organism; antisense oligonucleotides complementary to AAF76023-AAF76031 are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene product (which
Sequence 1032 BP; 303
                                                                                                                                                                                                                                                                                                                                      colonisation by vancomycin resistant enterococci and other clinically significant pathogens, and may be used for the ex vivo eradication of vancomycin-resistant enterococci from frequently colonised settings, such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                induces vanH promoter activity) is competitively
A; 197 C; 264 G; 268 T;
      0 U; 0 Other;
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뫄 S Matches Query Match ocal 494 Similarity 27; Conserv CCTATCCTGTTTTTGTTAAGCCGGCGC 27 CCTATCCTGTTTTTGTTAAGCCGGCGC 520 Conservative 100.0%; 100.0%; Score 27; DB 100.0%; Pred. No. 0.03 <u>,</u> Mismatches 0.03; 4: <u>.</u>. Length 1032; Indels 0 Gaps

0

RESULT 4 AAH01064 BXXX AAH01064 standard; DNA; 1218

AAH01064;

24-JUL-2001

(first entry)

Enterococcus gallinarum nucleotide sequence SEQ ID NO:1055.

Species specific; genus specific; family specific; probe; detection; identification, algal; archaeal; bacterial; fungal; parasitical; microorganism; diagnosis; translation elongation factor Tu; toxin; translation elongation factor G; RecA recombinase; resistance; primer; catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;

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WO200123604-A2
                   Enterococcus gallinarum
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28-SEP-1999; 19-MAY-2000; 28-SEP-2000; 2000WO-CA001150 05-APR-2001. 99CA-02283458 2000CA-02307010

(INFE-) INFECTIO DIAGNOSTIC (IDI) INC. Boissinot M, Huletsky A, Menard C,

Ouellette

X

Bergeron MG, Picard FJ, ş

Example; Page 52; 59pp; English Reducing vancomycin-resistance in vancomycin-resistant introducing a antisense vancomycin-resistance molecule vancomycin-resistance gene expression, or by enhancing

organism by vanH

promoter

2001-211216/21

2001-245006/25

a repertory of

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AAHOIOA S

AAHOIOA S

AAHOIOA S

AC AAHO

AC AAA
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CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasitical species, genus, family and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungi and
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection
CC detection and for identification of Streptococcus pneumoniae. (I) obtained
CC gene. hexa nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC using the method of the invention can be used for the galanst
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC corynabacterium sp., Enterobacteriaceae group, Escherichia coli,
CC corynabacterium sp., Enterobacteriaceae group, Streptococcus sp., Neisseria
CC genules than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. Abi00100 to Abi002304
CC represent nucleotide sequences and primers/probes which are given in the
CC corynabacteriaceae family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species specific; genus specific; family specific; probe; detection; identification; algal; archaeal; bacterial; fungal; parasitical; microorganism; diagnosis; translation elongation factor Tu; toxin; translation elongation factor G; RecA recombinase; resistance; catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal bacterial, fungal and parasitical species in a test sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                       28-SEP-1999;
19-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH01063 standard; DNA; 1232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1218 BP;
                                                                                                                                                  28-SEP-2000; 2000WO-CA001150
                                                                                                                                                                                                                                                                                                            WO200123604-A2
                                                                                                                                                                                                                                                                                                                                                                                   Enterococcus faecalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dв.
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                                           99CA-02283458
2000CA-02307010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               faecalis nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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100.0%; 100.0%;

Score 27; Pred. No. Mismatches

0.031; 멂

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Indels

0

Gaps

0

4; Length 1218;

0;

BP

SEQ ID NO:1054.

WO200123604-A2

364 A; 226 C; 311 G; 317 T; 0 U; 0 Other;

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RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a method for generating a repertory of nucleic acids of tuf, fus, atpD and/or recA genes from which probes CC and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more CC related microorganisms e.g. algae, archaea, bacteria, fungi and can be used for universal detection and for specific and ubiquitous CC detection and identification of an algal, archaeal, bacterial, fungal and parasitical species, genus, family and group. A nucleic acid (I) obtained CC using the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the detection of at least one antimicrobial agent resistance gene or at least one toxin certain species or genus or family or phylum or group which can be detected include Abiotrophia adiacens, Bordetella sp., CC orynebacterium sp., Enterobacteriaceae group, Escherichia coli, Consubacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria con results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved. AAH00010 to AAH002304 represent nuclectide sequences and primers/probes which are given in the companies.
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Matches
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Best Local :
                                                                                                                                                  Species specific; genus specific; family specific; probe; detection; identification; algal; archaeal; bacterial; fungal; parasitical; microorganism; diagnosis; translation elongation factor Tu; toxin; translation elongation factor G; RecA recombinase; resistance; catalytic subunit of proton-translocating ATPase; antimicrobial; vaccatalytic subunit of proton-translocating ATPase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal bacterial, fungal and parasitical species in a test sample.
                                                                                                                                                                                                                                                                     Enterococcus faecium nucleotide sequence SEQ ID NO:1052
                                                                                                                                                                                                                                                                                                              24-JUL-2001
                                                                                                                                                                                                                                                                                                                                                     AAH01061;
                                                                                                                                                                                                                                                                                                                                                                                         AAH01061 standard; DNA; 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1232 BP; 367 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 27; Page 1001; 1580pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bergeron MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
                                                                                             Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-245006/25
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                                                                                                                                   dв.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boissinot M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 27;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Huletsky A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               313 G; 323 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
0.031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Menard C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1232;
                                                                                                                                                        antimicrobial; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouellette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            algal, archaeal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a method for generating a repertory of concleic acids of tuf, fus, atpb and/or recA genes from which probes conditions of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be cused for producing probes and/or primers for detecting one or more crelated microorganisms e.g. algae, archaea, bacteria, fungi and congrassitical species, for universal detection and for specific and ubiquitous conference of the method of the invention can be used for the universal detection and consistical species, genus, family and group. A nucleic acid (I) obtained conference of any bacteriam, fungis or parasitie in a sample and for the detection of at least one antimicrobial agent resistance gene or at least one toxin conference of the method of the invention can be used for the universal detection of at least one antimicrobial agent resistance gene or at least one toxin conference of the detection and for identification of Streptococcus pneumoniae. (I) can be considered to design a therapeutic agent which is effective against conference of microorganisms. Microbial species or genus or family or phylum or group which can be detected include Abiotrophia adiacens, Bordetella sp., conference family, Pseudomonads group, Escherichia coli, conference family co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal bacterial, fungal and parasitical species in a test sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-SEP-1999;
19-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1237 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 27; Page 999; 1580pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
                                                                                                                                                                                        Enterococcus
                                                                                                                                                                                                                               24-JUL-2001
                                                                                                                                                                                                                                                                                                               AAH01058 standard; DNA; 1241
                                         catalytic
primer; ds
                                                                                                   microorganism;
                                                                                                                         Species specific; identification; a
                                                                                translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                      590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                      CCTATCCTGTTTTTGTTAAGCCGGCGC 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTATCCTGTTTTGTTAAGCCGGCGC 27
                                                        pecific; genus specific; family specific; probe; detection ation; algal; archaeal; bacterial; fungal; parasitical; nism; diagnosis; translation elongation factor Tu; toxin; on elongation factor G; RecA recombinase; resistance; subunit of proton-translocating ATPase; antimicrobial; vs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99CA-02283458.
2000CA-02307010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                      faecium nucleotide sequence
                                                                                                                                                                                                                             (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boissinot M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; 235 C; 314 G; 322 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 27;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                        SEQ ID NO:1049.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                 antimicrobial; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouellette
                                                                                                                                                 detection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    faster
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Enterococcus faecium

RESULT 8 AAH01059

standard; DNA; 1249

Enterococcus

gallinarum nucleotide sequence

SEQ ID

NO:1050

microorganism;

diagnosis;

translation

Species specific; genus specific; family specific; probe; detection; identification; algal; archaeal; bacterial; fungal; parasitical;

24-JUL-2001

(first entry)

AAH01059; AAH01059 S

CCTATCCTGTTTTTGTTAAGCCGGCGC 27

587

Matches Query Match Best Local

Conservative

ç

<u>.</u>

Indels

0,

Gaps

0

100.0%;

Score 27; D Pred. No. 0. Mismatches

띪 .031;

> Length 1241; U; 0 Other;

Sequence

1241 BP; 371 A;

228 C; 317 G; 325

T; 0 4.

밁

561 μ 27; Similarity

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The present invention describes a method for generating a repertory of concleic acids of tuf, fus, atpD and/or recA genes from which probes conditions are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be cused for producing probes and/or primers for detecting one or more created microorganisms e.g. algae, archaea, bacteria, fungi and comparasitical species, for universal detection and for specific and ubiquitous comparasitical species, genus, family and group. A nucleic acid (I) obtained cusing the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the detection of at least one antimicrobial agent resistance gene or at least one toxin certain the method of the detection of streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against corresponding a therapeutic agent which is effective against corresponding and include Abiotrophia adiacens, Bordetella sp., corresponding sp., Enterobacteriaceae group, Escherichia coli, corresults than substrate specificity tests as results can be determined in corresponding sp., also achieved. Abiotol to AbH002304 crepresent nucleotide sequences and primers/probes which are given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal bacterial, fungal and parasitical species in a test sample.
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19-MAY-2000; 2000CA-02307010.
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Best Local :
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A FJ, Roy PH;
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19-MAY-2000; 2000CA-02307010.
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                  24-JUL-2001
                                                                                            AAH01062 standard;
                                                                                                                                                                                                                                                                                                                                              Sequence 1249 BP; 373 A; 235 C; 316 G; 325 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 27; Page 998; 1580pp; English.
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                                                      AAH01062;
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                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                     Conservative
                (first entry)
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                                                                                          DNA; 1263
                                                                                                                                                                                         TTTTGTTAAGCCGGCGC 616
                                                                                                                                                                                                                                                                                        100.0%;
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RESULT 10 AAH01065 ID AAH01

AAH01065 standard; DNA; 1265

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Matches
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                                                                                                                                                                                                                                      Corynebacterium sp., Enterobacteriaceae group, Escherichia coli, Mycobacteriaceae family, Pseudomonads group, Streptcocccus sp., Neisseria gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved. AAH00010 to AAH002304 represent nucleotide sequences and primers/probes which are given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  species with a combination of defined primer pairs. The method can used for producing probes and/or primers for detecting one or more related microorganisms e.g. algae, archaea, bacteria, fungi and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal bacterial, fungal and parasitical species in a test sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a method for generating a repertory of nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-245006/25.
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19-MAY-2000; 2000CA-02307010.
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                                                                                                                                                                          Sequence
                                                                                                                                                                                                                   exemplification of the present invention
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                                                                                                           Local
582
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27; Conserv
                                        CCTATCCTGTTTTTGTTAAGCCGGCGC 27
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CCTATCCTGTTTTTGTTAAGCCGGCGC 608
                                                                                 100.0%; Score 27; Dilarity 100.0%; Pred. No. 0.0 Conservative 0; Mismatches
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Best Local
                      Sequence 1265 BP;
592
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              Similarity
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CCTATCCTGTTTTTGTTAAGCCGGCGC
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llarity 100.0%;
Conservative
                      379 A; 237 C; 320 G; 329 T; 0 U; 0 Other;
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           Mismatches
              No.
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Query Match Best Local Similarity

100.0%;

Score 27; Pred. No.

DB 4; 0.031;

Length 1269 0 Other;

Sequence 1269 BP; 380 A; 238 C; 321 G; 330 T; 0

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cc related microorganisms e.g. algae, archaea, bacteria, fungi and cc parasites, for universal detection and for specific and ubiquitous cd detection and identification of an algal, archaeal bacterial, fungal and cc detection and identification of an algal, archaeal bacterial, fungal and cc garasitteal species, genus, family and group. A nucleic acid (I) obtained cc using the method of the invention can be used for the universal detection cc of any bacterium, fungus or parasite in a sample and for the detection of cc at least one antimicrobial agent resistance gene or at least one toxin cc gene. hexA nucleic acids are used for the specific and ubiquitous cc detection and for identification of Streptococcus pneumoniae. (I) can be cc used to design a therapeutic agent which is effective against cc microorganisms. Microbial species or genus or family or phylum or group which can be detected include Abiotrophia adiacens, Bordetella sp., cc which can be detected include Abiotrophia adiacens, Bordetella sp., cc which can be detected include Abiotrophia adiacens, Bordetella sp., cc which can be detected include Abiotrophia Bordetella sp., Neisseria cc mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria cc gonorrhoeae and Staphylococcus sp. Using DNA based tests provides faster cresults than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved. AAH00010 to AAH002304 crepresent nucleotide sequences and primers/probes which are given in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid sequences are used to generate universal probes and which can be used to identify and detect the presence of algal, a bacterial, fungal and parasitical species in a test sample.
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19-MAY-2000;
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    exemplification of
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2000CA-02307010.
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        invention
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archaeal,
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RESULT 11
AAH01066
ID AAH01
                        Crelated microorganisms e.g. algae, archaea, bacteria, fungi and detection and independent of an algal, archaeal, bacterial, fungal and contection and identification of an algal, archaeal, bacterial, fungal and contection and identification of an algal, archaeal, bacterial, fungal and contection and identification of an algal, archaeal, bacterial, fungal and contection and pacterium, fungus or parasite in a sample and for the detection of content and incredible and sent resistance gene or at least one toxin of contection and for identification of streptococcus pneumoniae. (I) can be contection and for identification of streptococcus pneumoniae. (I) can be contection and for identification of streptococcus pneumoniae. (I) can be contection and for identification of streptococcus pneumoniae. (I) can be considered include Abiotrophia adiacens, Bordetella sp., contection be detected include Abiotrophia adiacens, Bordetella sp., contection sp., meterobacteriaceae group, Escherichia coli, contection sp., meterobacteriaceae group, Escherichia coli, contection sp., meterobacteriaceae group, Streptococcus sp., Neisseria contection sp., meterobacteriaceae group, Streptococcus sp., Neisseria contection sp., meterobacteriaceae group, Escherichia coli, contection sp., meterobacteriaceae group, streptococcus sp., Neisseria contection sp., meterobacteriaceae group, streptococcus sp., Neisseria content to such sp., value in the content sp., contection sp., meterobacteriaceae group, streptococcus sp., Neisseria contection sp., meterobacteriaceae group, streptococcus sp., neisseria contection sp., meterobacteriaceae group, streptococcus sp., neisseria contection sp., neis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more related microorganisms e.g. algae, archaea, bacteria, fungi and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid sequences are used to generate universal probes which can be used to identify and detect the presence of algobacterial, fungal and parasitical species in a test sample.
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19-MAY-2000;
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                 The present invention describes a method for generating a repertory of CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic CC acids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be CC used for producing probes and/or primers for detecting one or more CC used for producing probes and/or primers for detecting one or more CC related microorganisms e.g. algae, archaea, bacterial, fungal and general detection and for specific and ubiquitous CC detection and identification of an algal, archaeal, bacterial, fungal and CC parasitical species, genus, family and group. A nucleic acid (I) obtained CC using the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the detection of at least one antimicrobial agent resistance gene or at least one toxin CC detection and for identification of Streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against which to effective against which can be detected include Abiotrophia addacens, Bordetella sp., CC Corynebacteriaceae family. Pseudomonads group, Streptococcus sp., Neisseria gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster cesults than substrate specificity tests as results can be determined in continue and improved accuracy is also achieved. AAH00010 to AAH002304 represent nucleotide sequences and primers/probes which are given in the
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                          The present invention describes a method for generating a repertory of nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic coacids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be cused for producing probes and/or primers for detecting one or more created microorganisms e.g. algae, archaea, bacteria, fungi and corparasites, for universal detection and for specific and ubiquitous concentrated and concentrated and concentrated and concentrated and concentrated concentrated and concentrated an
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal, bacterial, fungal and parasitical species in a test sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    identification; algal; archaeal; bacterial; fungal; parasitical; microorganism; diagnosis; translation felongation factor Tu; toxin; translation elongation factor G, RecA recombinase; resistance; catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1272 BP; 379 A; 232
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19-MAY-2000; 2000CA-02307010.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure;
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d include www.--- Bachericumu Enterobacteriaceae group, Eschericumu Enterobacteriaceae group, Streptococcus
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k; Pred. No. 0.0
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Menard C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
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Mycobacteriaceae

RESULT 14 ADO47257 밁 8 ន្តន្តន្តន្តន្ត្ resistant enterococci (VRE) in a sample, comprising performing a cycling crep by amplifying a sample with pair of vanA or vanB primers and chybridising the sample with pair of vanA or vanB primers and comprising the sample with pair of vanA or vanB primes, labelled with chybridising the sample with pair of vanA or vanB primes, detecting donor and acceptor fluorescent group, respectively, detecting creinficture, the presence of the probes of the presence of the probes of the presence or absence of the presence or absence of the presence or absence of the method of the presence or absence of the method of the presence of the presence or absence of the method of the presence of the presence of the presence of the presence of the method of the presence of the Matches gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved. AAH00010 to AAH002304 represent nucleotide sequences and primers/probes which are given in the exemplification of the present invention Sequence 1768 BP; 537 A; 336 C; 437 G; 458 T; 0 U; 0 Other; Disclosure; SEQ ID NO 10; 23pp; English. Detecting presence or absence of vancomycin-resistant enterococci in biological sample from individual comprises using real time polymera WPI; 2004-268785/25 Cockerill FR, Sloan 25-SEP-2002; 2002US-00254260. 25-SEP-2002; 2002US-00254260 25-MAR-2004. US2004058336-A1. Enterococcus faecium. gene; ds; ho fluorescence Vancomycin resistant enterococcus; vancomycin resistance gene; vanA; gene; ds; hospital acquired infection; VRE; 15-JUL-2004 ADO47257 ADO47257 standard; DNA; 1768 The invention relates (SLOA/) SLOAN L M. faecium vancomycin resistance Jocal 870 27; Similarity CCTATCCTGTTTTTGTTAAGCCGGCGC 27 CCTATCCTGTTTTTGTTAAGCCGGCGC 896 Conservative (first entry) acquired 100.0%; ¥ to detecting the presence or absence of vancomycin-0 ; Score 27; DB; Pred. No. 0.0 먥 gene, vanA. 0.033; 멂 4: using real time polymerase 0; Length 1768; Indels <u>,,</u>

Query Match Best Local S Matches 27 RESULT 15 ADY59927 밁 S complement or portion, where the oligonucleotide hybridizes under stringent hybridization conditions to vanA or vanB DNA; and (2) a kit comprising one or more oligonucleotide(s) specific for a vanA gene and/or vanB gene in a test sample, comprising the oligonucleotide mentioned above. The method and kit are useful for detecting and/or amplifying genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying antibiotic resistance genes (e.g. vancomycin-resistant enterococcus). They may also be used in other industrial purposes, such as for quality control of food, water, pharmaceucical products or other products requiring microbiological control. The present sequence represents an Enterococcus faecium vanA nucleotide sequence from the present invention. 02-JUN-2005 ADY59927 oligonucleotide composition comprising a first oligonucleotide comprising sequences substantially corresponding to nucleotides 870-896, 851-868 or probe or primer, and detecting or determining the presence or amount hybrid formation or amplified nucleic acid. Also described: (1) an The invention relates to a method for detecting vancomycin resistance gene vanA and/or vanB nucleic acid molecules in a sample comprising contacting the sample with a vanA- and/or vanB-specific oligonucleotide Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for 12-SEP-2003; 2003US-00661094 US2005058985-A1 Enterococcus faecium vanA DNA sequence SEQ ID ADY59927 standard; 898-917 of the vanA gene, or its complement or portion, or an oligonucleotide comprising sequences substantially corresponding nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its Example 1; SEQ ID NO 1; 33pp; English. WPI; 2005-222218/23. Dodgson KJ; 12-SEP-2003; 2003US-00661094 17-MAR-2005 Enterococcus faecium. DNA detection; (DODG/) DODGSON K J identifying vancomycin-resistant enterococcus, com or vanB-specific oligonucleotide probes or primers. 870 1 CCTATCCTGTTTTTGTTAAGCCGGCGC Similarity CCTATCCTGTTTTTGTTAAGCCGGCGC 896 Conservative (first entry) antibiotic-resistance; vancomycin; vanA; gene; DNA; 1768 100.0%; Score 27; DB 12 Pred. No. 0.033; Mismatches 27 12; Length 1768; Indels comprises using vanA-0; ds. Сарв ç and/or œ, 0

Sequence 1768 BP; 537 A; 336 C; 437 G; 458

ď,

0 Other;

Matches Query Match

27;

Conservative

Local

Similarity

100.0%; 0

Pred. No. Score 27;

0.033; DB 14; T; 0

Length 1768;

Mismatches

0

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Gaps

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vanA,

vancomycin

resistance

537 A;

336 C; 437

<u>ი</u>

458 T;

0 U;

0 Other;

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AAT28569;
                                            AAT28569 standard; DNA;
                                                                                                      870
                                                                                                     CCTATCCTGTTTTTGTTAAGCCGGCGC 896
(first entry)
                                             2607
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Bacterial antibiotic resitance gene, vanH, vanA and vanX, probe

Proteus mirabilis; Streptococcus pneumoniae; Staphylococcus aureus; Staphylococcus epidermidis; Enterococcus faecalis; respiratory tract; Staphylococcus saprophyticus; Streptococcus pyogenes; urinary tract; Staphylococcus saprophyticus; Streptococcus pyo Haemophilus influenzae; Moraxella catarrhalis; Detection; probe; amplification primer; bacterial pathogen; pneu Escherichia coli; Klebsiella pneumoniae; Pseudomonas aeruginosa; bacterial resistance; beta-lactam antibiotic; infection; intra-abdominal infection; skin infection; septicaemia; meningitis; pneumonia;

21-MAR-1996 WO9608582-A2

Synthetic

12-SEP-1995; 95WO-CA000528.

12-SEP-1994; 94US-00304732.

(BERG/) BERGERON M G. (OUEL/) OUELLETTE M. (ROYP/) ROY P H.

Bergeron MG, Ouellette Z, Roy PH

Method for the detection of bacterial species using probes and primers allows detection and quantification of antibiotic resistant bacteria in patients, the environment and food.

94; Page 145-147; 216pp; English.

The sequences given in AAT28560-76 represent fragments derived from CC bacterial antibiotic resistance genes which were used as probes in the CC method of the invention for the detection of bacterial species in a CC sample. The method of the invention comprises using probes and/or CC amplification primers which are specific, ubiquitous and sensitive for CC determining the presence and/or amount of nucleic acids from selected bacterial species in any sample, where the bacterial nucleic acid CC comprises a selected target region hybridisable with the probes or CC primers and detecting the presence and/or amount of hybridised primers or CC primers and detecting the presence and/or amount of hybridised primers or CC maplification products as and indication of the presence and/or amount of the bacterial species. This method may be used to detect commonly CC encountered bacterial pathogens, e.g. Escherichia coli, Klebsiella CC pneumoniae, Pseudomonas aeruginosa, Proteus mirabilis, Streptococcus groundiae, Staphylococcus aureus, Staphylococcus epidermidis, CC Enterococcus faecalis, Staphylococcus saprophyticus, Streptococcus grounding species are associated with approx. 90% of urinary tract CC including septicaemia, menningitis, pneumonia, intra-abdominal infections, CC skin infections and other severe respiratory tract infections. The method contral also be used to evaluate a bacterial resistance to beta-lactam may also be used to antibiotics

Sequence 2607 BP; 768 A 506 ü 652 <u>ن</u> 681 ij 0 Ģ 0 Other

Query Match Best Local S Matches 27

l Similarity 27; Conserv

Conservative

100.0%; 0

Score 27; DB Pred. No. 0.0 0; Mismatches

0.035; DB 4;

Length 2607;

0

Indels

0

Gaps

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RESULT 17
                                 The invention relates to detecting target bacterial species suspected to be present in a sample, comprising contacting nucleic acids of target CC bacterial by fragment (ABA7685-ABA77861) specific for the target bacterial by fragment (ABA7685-ABA778661) specific for the target CC bacterial by fragment (ABA7685-ABA76861) specific for the target bacterial species but ubiquitous for different strains, amplifying the concleic acid and detecting the presence or amount of an amplified CC sequence as an indication of the presence or amount of the target bacterial species. The invention includes primers and probes (ABA76862-ABA76984) against the target bacterial species amount of the target bacterial species. S. espidally E. Coli, CC k.pneumoniae, P. aeruginosa, P. mirabilis, S. pneumoniae, S. aureus, CC s. epidermidis, E. faecalis, S. saprophyricus, S. pyogenes, H. influenzae, CC k.pneumoniae, P. aeruginosa, P. mirabilis, S. pneumoniae, S. aureus, CC A., suspected to be present in a sample which is obtained from human compations of the present of cod, and which consists of one or more patients, animals, environment or food, and which consists of one or more bacterial genes encoding resistance to antibiotics such as bla(tem), CC the bacterial genes encoding resistance to antibiotics such as bla(tem), CC vanX, satA, aacA-aphD, vat, vga, msrA, sul and/or int (ABA76985-ABA77001) care also useful to identify commonly encountered and clinically important cresistance genes. The invention provides a rapid method of bacterial colonitics invention provides a rapid method of bacterial colonitics invention provides a rapid method of bacterial colonitics in the identification of pathogens in the clinical laboratory
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Best Local S
Matches 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Method for detecting target bacterial species in a sample, detecting the presence or amount of bacterial nucleic acid primer derived from bacterial DNA, specific for the target
Sequence 2607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 16; Page 160-162; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-615034/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bergeron MG, Ouellette M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-SEP-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IDII-) IDI INFECTIO DIAGNOSTIC INC
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BP; 768 A; 506 C; 652 G; 681 T; 0 U; 0 Other;
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Pred. No. 0.035;
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RESULT 18
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                                                                                                                                                                                                                                                                                                                                                                   translation elongation factor G; RecA catalytic subunit of proton-translocat
                                                                                                                                                                                                                                                                                                                                                                          identification; algal; archaeal; bacterial; fungal; parasitical; microorganism; diagnosis; translation elongation factor Tu; toxin; translation elongation factor G; RecA recombinase; resistance;
                                                                                                                                                                                                                                                                                                                                                                                              Species specific; genus specific; family specific; probe; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                           24-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH01150
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH01150 standard;
                                                                                                                                                                                                                                                                                                                                               Enterococcus faecium.
                                                                                                                                                                                                                                                                                                                                                                                                             Enterococcus faecium nucleotide sequence SEQ ID NO:1141.
                                                                                                                                                                                                                                                                                                                                                                                         dentification;
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                                                                                                                                                                                                                                                                                                                                                                     proton-translocating ATPase; antimicrobial; vaccine;
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28-SEP-2000; 2000WO-CA001150 05-APR-2001 WO200123604-A2

28-SEP-1999; 99CA-02283458 19-MAY-2000; 2000CA-02307010

(INFE-) INFECTIO DIAGNOSTIC (IDI) INC.

Picard FJ, Bergeron MG, Roy Boissinot M, Huletsky A, Menard C, Ouellette M;

Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal, bacterial, fungal and parasitical species in a test sample.

Disclosure; Page 1035-1036; 1580pp; English.

of any bacterium, fungus or parasite in a sample and for the detection of at least one antimicrobial agent resistance gene or at least one toxin gene. hexh nucleic acids are used for the specific and ubiquitous detection and for identification of Streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against microorganisms. Microbial species or genus or family or phylum or group which can be detected include Abiotrophia adiacens, Bordetella sp., Corynebacterium sp., Enterobacteriaceae group, Escherichia coli, Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria gonorrhoeae and Staphylococcus sp. Using DNA based tests provides faster results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved. AAH00010 to AAH002304 nucleic acids of tuf, fus, atpb and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more related microorganisms e.g. algae, archaea, bacteria, fungi and parasites, for universal detection and identification of an algal, archaeal, bacterial, fungal and parasitical species, genus, family and group. A nucleic acid (I) obtained using the method of the invention can be used for the universal detection represent nucleotide sequences and primers/probes which are given in the exemplification of the present invention invention describes a method for generating a repertory of fus, atpD and/or recA genes from which probes

RESULT 20 AAQ25178 ID AAQ25

AAQ25178 standard; DNA; 10851 BP

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AAQ25178;

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RESULT 19
AAQ25183
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25-MAR-2003
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                                                                                                                                                                                                                                 Polypeptides involved in expression of glycopeptide antibiotic resistance - useful in diagnosing presence of Gram-positive enterococcal strains e.g. Enterococcus Faecium and E Gallinarum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ25183 standard;
                                                                                                                     This sequence contains the genes vanH, vanA, vanX, vanR and vanS. The proteins encoded by the latter two genes (i.e. proteins VanR and VanS) have a regulatory function and control expression of the other three ("protective") proteins. See also AAQ25179-Q25182. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PI field (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycopeptide antibiotic; vancomycin; teicoplanin; resistant; D-Ala-D-Ala ligase; peptidoglycan precursor; transposon;
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                                                                                                Sequence 7227 BP; 2313 A; 1305 C; 1596 G;
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 CCTATCCTGTTTTTGTTAAGCCGGCGC 5044
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No. 0.037;
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Pred. No. 0.04;
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                      Polypeptides involved in expression of glycopeptide antibiotic resistance - useful in diagnosing presence of Gram-positive enterococcal strains e.g. Enterococcus Faecium and E Gallinarum.
                                                                                                                                                                                                                                                        CDS
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       Claim 9;
                                                                       WPI; 1992-183677/22
                                                                                                                                                        14-MAY-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_unit
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                                                                                       Arthur M,
                                                                                                                                       29-OCT-1991;
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                                                      AAR24294, AA
0, AAR24301,
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      Fig
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                                                                                       Dukta-Malen S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "transposase"
/note= "coded by the (-) strand - see AAQ25179"
                                                                                                                                                                                              /*tag=
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                                                                                                                                                                                     rpt_type= INVERTED
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The invention relates to methods of reducing vancomycin resistance in a CC vancomycin-resistant organism. One method involves introducing a CC vancomycin resistant organism. One method involves introducing a CC vancomycin resistance gene antisense mucleic acid into the organism; CC antisense oligonucleotides complementary to AAF76023-AAF76031 are graticularly preferred for this purpose. The second method involves CC providing additional vanH promoter sequences which are not operatively CC coupled to a vancomycin resistance gene, so that the phosphorylated vank gene product (which induces vanH promoter activity) is competitively CC sequestered. Both methods are able to restore antibiotic susceptibility in glycopeptide resistant enterococci. The methods of the invention are cuseful for reducing vancomycin resistance in a vancomycin resistant corganism, particularly Enterococcus faecium and Enterococcus ge. and Streptococcus sp., to which Enterococcus faecium and Enterococcus ge. and CC streptococcus sp., to which Enterococcus faecium and Enterococcus The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  competitive inducer sequestration; vanH promoter; vanR gene product; Enterococcus; Staphylococcus; Streptococcus; Gram-positive bacterium; antibiotic susceptibility; ex vivo eradication; in vivo eradication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reducing vancomycin-resistance in vancomycin-resistant introducing a antisense vancomycin-resistance molecule vancomycin-resistance gene expression, or by enhancing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expression.
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Matches 27
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25-OCT-2001;
08-FEB-2002;
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                                                                                                                                                                                                                                                                                                                                      New antisense nucleic acids, useful for identifying proteins or a for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-2002; 2002WO-US009107.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense; ds; prokaryotic essential gene; cell proliferation; drug design; gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vancomycin-resistant enterococci from frequently colonised settings, such as intensive care units, haemodialysis units, and chronic care facilities; for the in vivo clearance of vancomycin- resistant enterococci from colonised gastrointestinal or genitourinary tracts of animals, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  significant pathogens, and may be vancomycin-resistant enterococci
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                            The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the
                                                                                                                                                                                                                                                                             Claim 14;
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; 2001US-00948993.
; 2001US-0342923P.
; 2002US-00072851.
; 2002US-0362699P.
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                                                                                                             Length 110000;
                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                          Gaps
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RESULT 25
AD047264/c
ID AD047264 standard; DNA; 556 BP
XX
AC AD047264;
XX
DT 15-JUL-2004 (first entry)
XX
DT 15-JUL-2004 (first entry)
XX
Enterococcus vancomycin resist
XX
Vancomycin resistant enterococ
XY
Vancomycin resistant enterococ
XX
Vanc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X8X9X9X9X9X9X9X9X9X9X9X9X9X9X9X9X9X9X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to detecting the presence or absence of vancomycin-
CC resistant enterococci (VRE) in a sample, comprising performing a cycling
CC step by amplifying a sample with pair of vanA or vanB primers and
CC hybridising the sample with a pair of vanA or vanB probes, labelled with
CC donor and acceptor fluorescent group, respectively, detecting
CC fluorescence resonance energy transfer (FRET), where the presence of FRET
CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
CC and a donor fluorescent group and a corresponding fluorescent group. The
CC method is useful for detecting the presence of vanA or vanB probes
CC enterococci in a biological sample, e.g. stool samples, anal or
CC replaces standard culture methods and reduces the cost. The method
CC replaces rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanA comprised resistance cans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting presence or absence of vancomycin-resistant enterococci in biological sample from individual comprises using real time polymerase
                                                                                                                                                                                                                                        gene; ds; hospital acquired infection; VRE;
fluorescence resonance energy transfer; FRE
                                                                                                                                                                                                                                                                                                       Vancomycin resistant enterococcus; vancomycin resistance
                                                                                                                                                                                                                                                                                                                                                                   Enterococcus vancomycin resistance gene, vanB ENEVANB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 555 BP; 132 A; 161 C; 115 G; 145 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 20; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-268785/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cockerill FR, Sloan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-SEP-2002; 2002US-00254260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-SEP-2002; 2002US-00254260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2004058336-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enterococcal vanB, vancomycin resistance gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (COCK/) COCKERILL F R. (SLOA/) SLOAN L M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCTACCCTGTCTTTGTGAAGCCGGCAC 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTATCCTGTTTTTGTTAAGCCGGCGC 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                            resonance energy transfer; FRET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
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Pred. No. 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                       gene; vanB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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ARSSULT 26
AD047262/c
ID AD0472:
XX AD0472:
XX AD0472:
XX Vancom
XX Vancom
XX Vancom
XX Entero
X
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       method is useful for detecting the presence or absence of vancomycin-
resistant enterococci in a biological sample, e.g. stool samples, anal
perirectal swabs, blood and body fluids from an individual. The method
replaces standard culture methods and reduces the cost. The method
provides rapid vancomycin resistant enterococcus real time PCR assay
which is useful for beginning the antimicrobial therapy immediately to
treat hospital acquired infection. The present sequence is an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E. faecalis vancomycin resistance gene, vanB EFU94526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADO47262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADO47262 standard; DNA; 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 556 BP; 130 A; 154 C; 117 G; 155 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 18; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting presence or absence of vancomycin-resistant enterococci in biological sample from individual comprises using real time polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-268785/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cockerill FR, Sloan LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-SEP-2002; 2002US-00254260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-SEP-2002; 2002US-00254260.
                                                                                                                                25-SEP-2002; 2002US-00254260
                                                                                                                                                                                              25-SEP-2002; 2002US-00254260.
                                                                                                                                                                                                                                                                                                                                                                                Enterococcus faecalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene; ds; hospital acquired infection; VRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chain reaction.
                                                                                                                                                                                                                                                             25-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (COCK/) COCKERILL F R. (SLOA/) SLOAN L M.
                                                                                                                                                                                                                                                                                                                        US2004058336-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  fluorescence
                                (COCK/) COCKERILL F R. (SLOA/) SLOAN L M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTACCCTGTCTTTGTGAAGCCGGCAC 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  resonance energy transfer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vanB, vancomycin resistance gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.3%;
85.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detecting the presence or absence of vancomycin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 20.6;
Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Detecting presence or absence of vancomycin-resistant enterococci in biological sample from individual comprises using real time polymerase

WPI; 2004-268785/25 Cockerill FR,

Sloan LM

The invention relates to detecting the presence or absence of vancomycin-resistant enterococci (VRE) in a sample, comprising performing a cycling step by amplifying a sample with pair of vanh or vanB primers and

hybridising the sample with a pair of vanA or vanB probes, labelled with donor and acceptor fluorescent group, respectively, detecting fluorescence resonance energy transfer (FRET), where the presence of FRET

Disclosure; SEQ ID NO 15; 23pp; English

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RESULT 27
ADO47263/c
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       Detecting presence or absence of vancomycin-resistant enterococci biological sample from individual comprises using real time polyme
                                                                                                             25-SEP-2002; 2002US-00254260
                                                                                                                                  25-SEP-2002; 2002US-00254260
                                                                                                                                                        25-MAR-2004
                                                                                                                                                                            US2004058336-A1
                                                                                                                                                                                                 Enterococcus faecalis.
                                                                                                                                                                                                                                       Vancomycin resistant enterococcus; vancomycin
                                                                                                                                                                                                                                                                                  15-JUL-2004
                                                                                                                                                                                                                                                                                                      ADO47263;
                                                                                                                                                                                                                                                                                                                            ADO47263 standard; DNA; 556 BP
                                        WPI; 2004-268785/25
                                                            Cockerill FR, Sloan
                                                                                                                                                                                                                    fluorescence
                                                                                (COCK/) COCKERILL F R. (SLOA/) SLOAN L M.
                                                                                                                                                                                                                                                              faecalis
                                                                                                                                                                                                                                                                                                                                                                               392
                                                                                                                                                                                                                               ds; hospital acquired infection;
reaction.
                                                                                                                                                                                                                                                                                                                                                                               CCTACCCTGTCTTTGTGAAGCCGGCAC 366
                                                                                                                                                                                                                                                            vancomycin resistance gene, vanB BFU94527.
                                                                                                                                                                                                                     resonance
                                                                                                                                                                                                                                                                                  (first entry)
                                                             Z
                                                                                                                                                                                                                    energy transfer; FRET
                                                                                                                                                                                                                                VRE;
                                                                                                                                                                                                                                         resistance
                                                                                                                                                                                                                                        gene; vanB;
        polymerase
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25-SEP-2002; 2002US-00254260 25-SEP-2002; 2002US-00254260

(COCK/) COCKERILL F R. (SLOA/) SLOAN L M.

The invention relates to detecting the presence or absence of vancomycin-resistant enterococci (VRE) in a sample, comprising performing a cycling step by amplifying a sample with pair of vanA or vanB primers and hybridising the sample with a pair of vanA or vanB probes, labelled with

Disclosure;

SEQ ID NO 14; 23pp; English

Detecting presence or absence of vancomycin-resistant enterococci in biological sample from individual comprises using real time polymerase

WPI; 2004-268785/25. Cockerill FR,

Sloan LM

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S
                                                         Matches
                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                    resistant enterococci (VRE) in a sample, comprising performing a cycling step by amplifying a sample with pair of vanA or vanB primers and hybridising the sample with a pair of vanA or vanB probes, labelled with donor and acceptor fluorescent group, respectively, detecting fluorescence resonance energy transfer (FRET), where the presence of FRET indicates presence of VRE. Also included is an article of manufacture,
                                                                                                                                                                                                                                                             comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes and a donor fluorescent group and a corresponding fluorescent group. The method is useful for detecting the presence or absence of vancomycin-resistant enterococci in a biological sample, e.g. stool samples, anal or perirectal swabs, blood and body fluids from an individual. The method replaces standard culture methods and reduces the cost. The method
                                                                                                                                                                                                 provides rapid vancomycin resistant enterococcus real time PCR assay which is useful for beginning the antimicrobial therapy immediately treat hospital acquired infection. The present sequence is an
                                                                                                                                        Sequençe 556 BP; 130 A; 154 C; 117 G; 155 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to detecting the presence or absence of vancomycin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 17; 23pp; English
                                                                                ocal.
                                                         23;
                                                                              Similarity
CCTATCCTGTTTTTGTTAAGCCGGCGC 27
                                                         Conservative
                                                                                                                                                                                vanB, vancomycin resistance gene.
                                                                          76.3%;
                                                         0;
                                                                              Score 20.6;
Pred. No. 2
                                                           Mismatches
                                                                                23;
                                                                                                    명
                                                                                                 12;
                                                         4
                                                                                                                                          0 Other;
                                                           Indels
                                                                                                 Length 556;
                                                                                                                                                                                                          immediately to
is an
                                                           0
                                                           Gaps
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                                                             0
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indicates presence of VRE. Also included is an article of manufacture, comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes and a donor fluorescent group and a corresponding fluorescent group. The method is useful for detecting the presence or absence of vancewcin-resistant enterococci in a biological sample, e.g. stool samples, anal or perirectal swabs, blood and body fluids from an individual. The method replaces standard culture methods and reduces the cost. The method provides rapid vancomycin resistant enterococcus real time PCR assay which is useful for beginning the antimicrobial therapy immediately to treat hospital acquired infection. The present sequence is an

õ

Matches Query Match Best Local :

23;

Conservative

0 Score Pred.

Mismatches ŏ. 20.6;

4;

0;

Gaps

0

밁

392

CCTACCCTGTCTTTGTGAAGCCGGCAC 366

DB 12;

Length Indels

CCTATCCTGTTTTTGTTAAGCCGGCGC 27

Similarity

76.3%; 85.2%;

Sequence 556 BP; 133 A; 162 C; 116 G; 145 T; 0 U; 0 Other;

enterococcal vanB, vancomycin resistance gene.

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RESULT 28
ADO47261/c
                                                                                                                                                 Vancomycin resistant enterococcus; vancomycin resistance gene; vanB; gene; ds; hospital acquired infection; VRB; fluorescence resonance energy transfer; FRET.
                                                                                                                                                                                                                                                      E. faecalis vancomycin resistance gene, vanB EFU94529.
                                                                                                                                                                                                                                                                                                                                                         ADO47261;
25-MAR-2004.
                                                 US2004058336-A1
                                                                                                  Enterococcus faecalis
                                                                                                                                                                                                                                                                                                          15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                             ADO47261 standard; DNA; 556 BP
                                                                                                                                                                                                                                                                                                          (first entry)
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RESULT 29
AD047265/c
ID AD0472
XX AD0472
XX AD0472
XX YANCOMM
KW Gene;
KW YANCOMM
KW Gene;
KW Fluore
XX US2004
XX US2004
XX (COCK)
PP 25-SEE
XX (COCK)
PA (SLOA)
XX (COCK)
PA (SLOA)
XX Detect
PT Chain
XX 
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Best Local S
Matches 23
The invention relates to detecting the presence or absence of vancomycin-resistant enterococci (VRE) in a sample, comprising performing a cycling step by amplifying a sample with pair of vanA or vanB primers and hybridising the sample with a pair of vanA or vanB probes, labelled with donor and acceptor fluorescent group, respectively, detecting fluorescence resonance energy transfer (FRET), where the presence of FRET indicates presence of VRE. Also included is an article of manufacture, comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes and a donor fluorescent group and a corresponding fluorescent group. The method is useful for detecting the presence or absence of vancomycin-resistant enterococci in a biological sample, e.g. stool samples, anal or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vancomycin resistant enterococcus; vancomycin resistance gene; vanB; gene; ds; hospital acquired infection; VRE_i fluorescence resonance energy transfer; FRET.
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     cc resistant enterococci (VRE) in a sample, comprising performing a cycling cc step by amplifying a sample with pair of vanA or vanB primers and cc hybridising the sample with a pair of vanA or vanB primers and cc donor and acceptor fluorescent group, respectively, detecting cc fluorescence resonance energy transfer (FRET), where the presence of FRET cc indicates presence of VRE. Also included is an article of manufacture, cc comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes cc and a donor fluorescent group and a corresponding fluorescent group. The cc method is useful for detecting the presence or absence of vanComycin-cc resistant enterococci in a biological sample, e.g. stool samples, anal or perisects standard culture methods and reduces the cost. The method cc provides rapid vancomycin resistant enterococcus real time PCR assay cc which is useful for beginning the antimicrobial therapy immediately to treat hospital acquired infection. The present sequence is an enterococcal vanB, vancomycin resistance gene.
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                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 13; 23pp; English
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resistant enterococci (VRE) in a sample, comprising performing a cycling
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                                                                                                                                                                                                                                                    resistant enterococci (VRB) in a sample, comprising performing a cycling step by amplifying a sample with pair of vanA or vanB primers and hybridising the sample with a pair of vanA or vanB probes, labelled with donor and acceptor fluorescent group, respectively, detecting fluorescence resonance energy transfer (FRET), where the presence of FRET indicates presence of VRE. Also included is an article of manufacture,
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                                                             Sequence 556 BP; 134 A; 161 C; 116 G; 145 T; 0 U;
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Pred. No. 23;
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                                 DB 12;
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 4.
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                                 Length 556;
                                                                  0 Other;
   Indels
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1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27

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RESULT 32
AAQ69230
ID AAQ69
RESULT 33
ADY59941
ID ADY59
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AC ADY59
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DT 02-JU
XX
DE Enter
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Best Local S
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                                                                                                                                                                                                                                                                         The protein encoded by the vanB gene is implicated in resistance of Gram-
positive bacteria to glycopeptides, particularly to vancomycin. This
resistance is inducible by Vancomycin but not by teicoplanin. Sequence
AAQ69230 is a claimed internal fragment of the vanB gene. (Updated on 25-
MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arthur M, Dutka-Malen S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterococcus faecalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gram positive teicoplanin; a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterococcus faecalis vanB gene (internal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
23-FEB-1995
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                                                                                                                                                                                                                                                                                                                                                                            New protein VanB involved in bacterial resistance to glyco-peptide(s) esp vancomycin, and related nucleic acid, vectors, transformed cells antibodies, for in vitro detection of resistant strains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FR2699539-A1
                                                                                                                                                                                                                                                                                                                                                    Claim 8; Page 28; 39pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1994-227159/28.
P-PSDB; AAR57150.
             Enterococcus faecalis vanB
                                     02-JUN-2005
                                                             ADY59941;
                                                                                     ADY59941 standard; DNA; 630
                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INSP ) INST PASTEUR
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                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                  CCTATCCTGTTTTTGTTAAGCCGGCGC
                                                                                                                                                   cciaccidiciiidigaagccggcac 191
                                                                                                                                                                                                                                                    589 BP;
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bacteria; inducible glycopeptide resistance; vancomycin;
antibiotic; vanB gene; ds.
                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92FR-00015671.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                    163 A; 124 C; 166 G; 136 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "amplified internal fragment of vanB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
                                                                                                                                                                                                              76.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      589
             DNA sequence SEQ ID NO:15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Evers
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                                                                                                                                                                                                    0;
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Pred. No. 23;
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                                                                                                                                                                                                                           Length 589
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ADY59942
ID ADY59
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ADY599
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AC ADY59
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O2-JT
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Enter
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KW DNA (
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OS Enter
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OS Enter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oligonucleotide composition comprising a first oligonucleotide comprising sequences substantially corresponding to nucleotides 870-896, 851-868 or 898-917 of the vanA gene, or its complement or portion, or an conjugation of the vanA gene, or its complement or portion, or an conjugation of the vanB gene, or its complement or portion, where the oligonucleotide hybridizes under the comprising sequences substantially corresponding to nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its complement or portion, where the oligonucleotide hybridizes under the comprising one or more oligonucleotide (s) specific for a vanA gene and/or comprising one or more oligonucleotide (s) specific for a vanA gene and/or vanB gene in a test sample, comprising the oligonucleotide mentioned cabove. The method and kit are useful for detecting and/or amplifying genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).

They may also be used in other industrial purposes, such as for quality control of food, water, pharmaceutical products or other products requiring microbiological control. The present sequence represents an extension of the present sequence from the present
                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contacting the sample with a vanA- and/or vanB-specific oligonucleotide probe or primer, and detecting or determining the presence or amount of hybrid formation or amplified nucleic acid. Also described: (1) an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-and/or vanB-specific oligonucleotide probes or primers.
                                                                                                                  Enterococcus
                                                                                                                                                     02-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene vanA and/or vanB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; SEQ ID NO 15; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-SEP-2003; 2003US-00661094.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterococcus faecalis.
 US2005058985-A1
                                       Enterococcus faecalis
                                                                                                                                                                                             ADY59942
                                                                                                                                                                                                                                ADY59942 standard; DNA; 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dodgson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-SEP-2003; 2003US-00661094.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
                                                                            DNA detection; antibiotic-resistance; vancomycin; vanB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DODG/)
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                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                             CCTACCCTGTCTTTGTGAAGCCGGCAC 211
                                                                                                                                                                                                                                                                                                                                                                   CCTATCCTGTTTTTGTTAAGCCGGCGC 27
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                  faecalis vanB
                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP; 163 A; 135 C; 187 G; 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        relates
                                                                                                                                                                                                                                                                                                                                                                                                                    76.3%;
85.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to a method for detecting vancomycin resistance nucleic acid molecules in a sample comprising
                                                                                                                DNA sequence
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Pred. No. 2
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                                                                                                                SEQ ID NO:16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0 Other;
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RESULT 35
AAH01126
ID AAH01
XX AAH01
XX AAH01
XX BAH01
XX Bect
XX Spect
XX 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      colligonization of comprising a first oligonization of colligonization of colligonization of comprising conspirations and conspiration of che vana gene, or its complement or portion, or an colligonization comprising sequences substantially corresponding to oligonization or its complement or portion, where the oligonization depends on its complement or portion, where the oligonization depends on the comprising sequences substantially corresponding to complement or portion, where the oligonization depends on the comprising one or more oligonization conditions to vana or vana plank, and (2) a kit comprising one or more oligonization of the vana of vana gene and/or vana gene in a test sample, comprising the oligonization conditions of collecting and/or applifying genes (i.e. vana and/or vana genes) in a test sample, or for identifying control of food, water, pharmaceutical products or other products or control of food, water, pharmaceutical products or other products or requiring microbiological control. The present sequence represents an and the control of food, water, pharmaceutical products or other products or other products or control of food, water, pharmaceutical products or other products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                  Species specific; genus specific; family specific; probe; detection; identification; algal; archaeal; bacterial; fungal; parasitical; microorganism; diagnosis; translation elongation factor Tu; toxin; translation elongation factor G; RecA recombinase; resistance; catalytic subunit of proton-translocating ATPase; antimicrobial; vac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH01126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH01126 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; SEQ ID NO 16;
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                                                                                                                                                                                                                                                                                                                                                                              Enterococcus faecium nucleotide sequence SEQ ID NO:1117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                            ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCTACCCTGTCTTTGTGAAGCCGGCAC 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.3%;
85.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; 166
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Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G; 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0 Other;
                                                                                                                                                                                antimicrobial; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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WO200123604-A2 Enterococcus faecium

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RESULT 36
ADY59937/c
ID ADY599
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PX SX XX BX PX PX X
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Best Local S
Matches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 801 BP; 215 A; 169 C; 235 G; 182 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acids of determined algal, accuracy, species with a combination of defined primer pairs. The method can species with a combination of defined primers for detecting one or more used for producing probes and/or primers for detecting one or more used for producing immage algae, archaea, bacteria, fungi and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a method for generating a repertory of nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 1027; 1580pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal, bacterial, fungal and parasitical species in a test sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-245006/25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-SEP-1999; 99CA-02283458.
19-MAY-2000; 2000CA-02307010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-SEP-2000; 2000WO-CA001150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exemplification of the present invention
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                                                                                                                                                     Enterococcus
                                                                                                                                                                                                      02-JUN-2005
                                                                                                                                                                                                                                                        ADY59937;
                                                                                                                                                                                                                                                                                                         ADY59937 standard; DNA; 801
                                                  Enterococcus faecium.
                                                                                                     DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                      389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTATCCTGTTTTTGTTAAGCCGGCGC 27
                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTACCCTGTCTTTGTGAAGCCGGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boissinot M, Huletsky A, oy PH;
                                                                                                                                                     faecium vanB DNA sequence SEQ ID NO:11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 20.6; D
Pred. No. 25;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Menard C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            멂
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 801;
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RESULT 37
ADY59940/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GC sequences substantially corresponding to nucleotides 870-896, 851-868 or CC 898-917 of the vanA gene, or its complement or portion, or an CC oligonucleotide comprising sequences substantially corresponding to CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its CC complement or portion, where the oligonucleotide hybridizes under CC comprising one or more oligonucleotide (s) specific for a vanA gene and/or CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or CC vanB gene in a test sample, comprising the oligonucleotide mantioned CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying CC entibiotic resistance genes (e.g. vancomycin-resistant enterococcus). CC control of food, water, pharmaceutical purposes, such as for quality CC control of food, water, pharmaceutical products or other products and control of food, water, pharmaceutical products or other products and control of food water, pharmaceutical products or other products and control of food water, pharmaceutical products or other products and control of food water, pharmaceutical products or other products and control of food water, pharmaceutical products or other products and control of food water, pharmaceutical products or other products and control of food water, pharmaceutical products or other products and control of food water, pharmaceutical products or other products and control of food water, pharmaceutical products or other products and control of food water, pharmaceutical products or other products and control of food water, pharmaceutical products or other products and control of food water, pharmaceutical products or other products and control of food water, pharmaceutical products or other products and control of con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a method for detecting vancomycin resistance gene vanA and/or vanB nucleic acid molecules in a sample comprising contacting the sample with a vanA- and/or vanB-specific oligonuclectide contacting the sample with a vanA- and/or vanB-specific oligonuclectide contacting the sample with a vanA- and/or vanB-specific oligonuclectide contacting the sample with a vanA- and/or vanB-specific oligonuclectide contacting the sample with a vanA- and/or vanB-specific oligonuclectide contacting the sample with a vanA- and/or vanB-specific oligonuclectide contacting the sample with a vanA- and/or vanB-specific oligonuclectide contacting the sample with a vanA- and/or vanB-specific oligonuclectide contacting the sample with a vanA- and/or vanB-specific oligonuclectide contacting the sample with a vanA- and/or vanB-specific oligonuclectide contacting the sample with a vanA- and/or vanB-specific oligonuclectide contacting the sample with a vanA- and/or vanB-specific oligonuclectide contacting the sample with a vanA- and/or vanB-specific oligonuclectide contacting the sample with a vanA- and/or vanB-specific oligonuclectide contacting the sample with a vanA- and/or vanB-specific oligonuclectide contacting the sample with a vanA- and/or vanB-specific oligonuclectide contacting the sample with a vanA- and/or vanB-specific oligonuclectide contacting the sample with a vanA- and/or vanB-specific oligonuclectide contacting the sample with a vanA- and/or vanB-specific oligonuclectide contacting the sample with a vanA- and/or vanB-specific oligonuclection of vanB-specific oligonucleum the sample with a vanA- and/or vanB-specific oligonucleum the sample with a vanA- and/or vanB-specific oligonucleum the vanA- and/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-and/or vanB-specific oligonucleotide probes or primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 801 BP; 181 A; 226 C; 169 G; 225 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oligonucleotide composition comprising a first oligonucleotide comprising enterprise state of the composition of the control o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; SEQ ID NO 11; 33pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DODG/) DODGSON K J.
                                                                                                    12-SEP-2003; 2003US-00661094.
                                                                                                                                                                                                                                                                                                                    US2005058985-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterococcus faecium vanB DNA sequence SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADY59940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADY59940 standard; DNA; 801 BP.
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                                                                                                                                                                                                               17-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                        Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTATCCTGTTTTTGTTAAGCCGGCGC
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85.2%;
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Pred. No. 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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12-SEP-2003; 2003US-00661094.

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ADY59943/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probe or prime, and detecting or determining the presence or amount of hybrid formation or amplified nucleic acid. Also described: (1) an oligonucleotide composition comprising a first oligonucleotide comprising sequences substantially corresponding to nucleotides 870-896, 851-868 or 898-917 of the vanA gene, or its complement or portion, or an oligonucleotide comprising sequences substantially corresponding to nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its complement or portion, where the oligonucleotide hybridizes under stringent hybridization conditions to vanA or vanB MA, and (2) a kit comprising one or more oligonucleotide(s) specific for a vanA gene and/or vanB gene in a test sample, comprising the oligonucleotide mentioned above. The method and kit are useful for detecting and/or amplifying genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying antibiotic resistance genes (e.g. vancomycin-resistant enterococcus) antibiotic resistance genes (e.g. vancomycin-resistant enterococcus) control of food, water, pharmaceutical products or other products an requiring microbiological control. The present sequence represents an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-and/or vanB-specific oligonucleotide probes or primers.
                                                                                                                                                                                                                                 Enterococcus
Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method for detecting vancomycin resistance gene vanA and/or vanB nucleic acid molecules in a sample comprising
                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                             02-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                              ADY59943;
                                                                                                                                                                                                                                                                                                                                                                                                                                  ADY59943 standard; DNA; 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 801 BP; 183 A; 234 C; 169 G; 215 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; SEQ ID NO 14; 33pp; English.
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Dodgson KJ
                                                                     12-SEP-2003; 2003US-00661094
                                                                                                        12-SEP-2003; 2003US-00661094.
                                                                                                                                                                             US2005058985-A1
                                                                                                                                                                                                                                                                                      DNA detection; antibiotic-resistance; vancomycin; vanB;
                                                                                                                                                                                                                                                                                                                         Consensus vanB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enterococcus faecium vanB nucleotide sequence from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contacting the sample with a vanA- and/or vanB-specific oligonucleotide
                                   (DODG/) DODGSON K J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DODG/) DODGSON K J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTACCCTGTCTTTGTGAAGCCGGCAC 387
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                                                                                                                                                                                                                                                      faecium.
                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                       DNA sequence SEQ ID NO:14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 20.6;
Pred. No. 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 801;
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Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
                                                                                                                                                                                                                    WPI; 2005-222218/23.
                                                                                                                                                                                        vanB-specific oligonucleotide probes
                                                                                                                                                                                              vancomycin-resistant enterococcus, comprises using vanA-
                                                                                                                                                                                        or primers.
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Example 1; SEQ ID NO 17; 33pp; English.

CC probe or primer, and detecting or determining the presence or amount of chybrid formation or amplified nucleic acid. Also described: (1) an CC oligonucleotide composition comprising a first oligonucleotide comprising cc sequences substantially corresponding to nucleotides 870-896, 851-868 or CC 898-917 of the vanA gene, or its complement or portion, or an CC oligonucleotide comprising sequences substantially corresponding to complement or portion, or an CC oligonucleotide 387-404, 406-423 or 426-446 of the vanB gene, or its complement or portion, where the oligonucleotide hybridizes under CC comprising one or more oligonucleotide hybridizes under CC comprising one or more oligonucleotide (s) specific for a vanA gene and/or vanB gene in a test sample, comprising the oligonucleotide mentioned CC above. The method and kit are useful for detecting and/or amplifying CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying CC control of food, water, pharmaceutical products or other products or control of food, water, pharmaceutical products or other products are products.

CC requiring microbiological control. The present sequence represents a The invention relates to a method for detecting vancomycin resistance gene vanA and/or vanB nucleic acid molecules in a sample comprising contacting the sample with a vanA- and/or vanB-specific oligonuclectide requiring microbiological control. The present sequence represents a consensus vanB nucleotide sequence from the present invention.

Sequence 801 BP; 181 A; 235 C; 169 G; 216 T; 0 U; 0 Other;

밁 S Matches Query Match Best Local (413 1 CCTATCCTGTTTTTGTTAAGCCGGCGC 27 23; Similarity CCTACCCTGTCTTTGTGAAGCCGGCAC 387 Conservative 76.3%; 85.2%; .. Score 20.6; Pred. No. 25; Mismatches B 14; Length 801; Indels 0 Gaps

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ADYS9939/c
ID ADYS993
AC ADCACH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADY59939 standard; DNA; 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2005058985-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA detection; antibiotic-resistance; vancomycin; vanB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterococcus faecium vanB DNA sequence SEQ ID NO:13
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12-SEP-2003; 2003US-00661094.

12-SEP-2003; 2003US-00661094

(DODG/) DODGSON K J.

WPI; 2005-222218/23.

Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-and/or vanB-specific oligonucleotide probes or primers.

SEQ ID NO 13; 33pp; English.

oligonucleotide comprising sequences substantially corresponding to nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its complement or portion, where the oligonucleotide hybridizes under stringent hybridization conditions to vanA or vanB DNA; and (2) a kit comprising one or more oligonucleotide(s) specific for a vanA gene and/or vanB gene in a test sample, comprising the oligonucleotide mentioned above. The method and kit are useful for detecting and/or amplifying genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying antibiotic resistance genes (e.g. vancomycin-resistant enterococcus). They may also be used in other industrial purposes, such as for quality control of food, water, pharmaceutical products or other products a requiring microbiological control. The present sequence represents an enterococcus faecium vanB nucleotide sequence from the present invention. The invention relates to a method for detecting vancomycin resistance gene vanA and/or vanB nucleic acid molecules in a sample comprising contacting the sample with a vanA- and/or vanB-specific oligonuclectide oligonucleotide composition comprising a first oligonucleotide comprising 898-917 of the vanA gene, or its complement or portion, or an sequences substantially corresponding to nucleotides 870-896, 851-868 probe or primer, and detecting or determining the presence or amount of hybrid formation or amplified nucleic acid. Also described: (1) an

Sequence 801 BP; 183 A; 234 C; 169 G; 215 T; 0 U; 0 Other;

ঠ Matches Best Local Similarity Query Match 23; ٠, CCTATCCTGTTTTTGTTAAGCCGGCGC 27 Conservative 76.3%; 85.2%; 0; Score 20.6; Pred. No. 25; Mismatches B 14; 4; Length 801; 0; Gaps

0

RESULT 40 ADY59936/c ADY59936; ADY59936 standard; DNA; 801 BP.

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413

02-JUN-2005 (first entry)

Enterococcus faecium vanB DNA sequence SEQ ID NO:10.

DNA detection; antibiotic-resistance; vancomycin; vanB; ds.

Enterococcus faecium

US2005058985-A1

17-MAR-2005

12-SEP-2003; 2003US-00661094.

12-SEP-2003; 2003US-00661094

(DODG/) DODGSON K J

Dodgson KJ;

WPI; 2005-222218/23.

Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-and/or vanB-specific oligonucleotide probes or primers.

Example 1; SEQ ID NO 10; 33pp; English

The invention relates to a method for detecting vancomycin resistance gene vanA and/or vanB nucleic acid molecules in a sample comprising contacting the sample with a vanA- and/or vanB-specific oligonucleotide

comprising one or more oligonucleotide(s) specific for a vanA gene and/or vanB gene in a test sample, comprising the oligonucleotide mentioned above. The method and kit are useful for detecting and/or amplifying genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying antibiotic resistance genes (e.g. vancomycin-resistant enterococcus). They may also be used in other industrial purposes, such as for quality control of food, water, pharmaceutical products or other products an requiring microbiological control. The present sequence represents an oligonucleotide comprising sequences substantially corresponding to nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its complement or portion, where the oligonucleotide hybridizes under stringent hybridization conditions to vanA or vanB DNA; and (2) a kit probe or primer, and detecting or determining the presence or amount of hybrid formation or amplified nucleic acid. Also described: (1) an oligonucleotide composition comprising a first oligonucleotide composition comprising to nucleotides 870-896, 851-868 or sequences substantially corresponding to nucleotides 870-896, 851-868 or Enterococcus faecium vanB nucleotide sequence from the present sequences substantially corresponding to nucleotides 870-896, 898-917 of the vanA gene, or its complement or portion, or an e comprising 851-868 or

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Sequence 801 BP; 182 A; 235 C; 169 G; 215 T; 0 U; 0 Other;

닭 S Query Match Best Local Matches 413 23; Similarity CCTATCCTGTTTTTGTTAAGCCGGCGC 27 CCTACCCTGTCTTTGTGAAGCCGGCAC 387 Conservative 76.3%; 85.2%; 0; Score 20.6; Pred. No. 25 Mismatches 멂 14; 4 Indels Length 801; 0 Gaps

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Search completed: April Job time : 381.134 secs 9, 2006, 06:41:33

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